

Snedden, S.
091881569

09/881569

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PR 14-OCT-1999: 99US-0159637.
PR 14-OCT-1999: 99US-0159638.
PR 18-OCT-1999: 99US-0159584.
PR 21-OCT-1999: 99US-0160741.
PR 21-OCT-1999: 99US-0160767.
PR 21-OCT-1999: 99US-0160768.
PR 21-OCT-1999: 99US-0160770.
PR 21-OCT-1999: 99US-0160814.
PR 21-OCT-1999: 99US-0160815.
PR 22-OCT-1999: 99US-0160980.
PR 22-OCT-1999: 99US-0160981.
PR 22-OCT-1999: 99US-0160989.
PR 25-OCT-1999: 99US-0161404.

XX Novel polycomb group nucleic acids and polypeptides from maize useful
PT for producing transgenic plants and to repress expression or prevent
PT the expression of a desired target gene in specific tissue in plants in
PT vivo -
XX
PS Claim 8: Fig 2B; 80pp; English.
XX
CC The invention relates to plant genetic engineering. More specifically,
CC the invention relates to isolated and purified polycomb group (PCG) genes
CC from 2ea mays (maize), termed Mez1 and Mez2 (Maize E12)-like 1 and 2)
CC genes comprising a sequence of 3180 and 3010 bp respectively, defined in
CC the specification, or its conservatively modified and polymorphic
CC variants. The PCG genes of the invention are useful in constructing
CC recombinant expression cassettes which can be introduced into a desired
CC plant, to produce a transgenic plant. Promoters derived from the Mez1 or
CC Mez2 genes are useful to direct expression of heterologous sequences. The
CC modified variants of the PCG genes are useful for generating or selecting
CC antibodies immunoreactive to the non-variant polypeptide and to follow
CC the segregation of chromosome regions and in marker assisted selection
CC methods for crop improvement. Mez1 and Mez2 proteins can be used to
CC repress the expression or prevent the expression of a desired target gene
CC in specific tissue in a plant in vivo, to regulate homeotic gene
CC expression in plants to create novel plants having improved agronomic
CC traits. Protein derived from a PCG gene of the invention is useful as an
CC immunogen for producing monoclonal or polyclonal antibodies which are
CC useful for screening plants for the expression of a Mez1 or Mez2
CC polypeptide, and for affinity chromatography for isolating a Mez1 or Mez2
CC polypeptide. This sequence represents the protein of Mez 2 of the
CC invention.
XX
SQ Sequence 893 AA:

Query Match 43.1%; Score 44; DB 23; Length 893;
Best Local Similarity 38.9%; Pred. NO. 95;
Matches 7; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 BRSZPCGAVMILYFHKR 18
: :||| :| :||
Db 317 ENKPCGHLCYLRFPQWR 334

RESULT 6
AAU78464
ID AAU78464 standard; Protein; 954 AA.
XX
AC AAU78464;
XX
DT 02-JUL-2002 (first entry)
XX
DE Sphingolipid ceramide deacylase.

Sphingolipid ceramide deacylase; nootropic; neuroprotective; cyrostatic;
vulnerary; neurodegenerative disease; leukaemia; wound; enzyme.
XX
OS Shewanella alga.
XX
PN WO200226963-A1.
XX
PD 04-APR-2002.
XX
PF 26-SEP-2001; 2001WO-JP08344.
XX
PR 26-SEP-2000; 2000JP-0293181.
XX
PA (TAKI) TAKARA SHUZO CO LTD.
XX
PI Ito M, Furusato M, Sueyoshi N;
XX
XX WPI; 2002-340011/37.
DR N-PSDB; ABK47644.
XX
PT New polypeptide with sphingolipid ceramide deacylase activity and

PT encoded gene, applicable in studying structure and function of
PT sphingolipid and its engineering for treatment of e.g.
PT neurodegenerative diseases and leukaemia -
XX
PS Example 6; Page 59-64; 89pp; Japanese.
XX
CC The invention relates to a polypeptide with sphingolipid ceramide
CC deacylase activity and its encoding nucleic acid. The polypeptide and its
CC encoded gene are applicable in studying structure and function of
CC sphingolipid and its engineering for treatment of e.g. neurodegenerative
CC diseases, leukaemia and wounds. The present sequence represents the
CC amino acid sequence of sphingolipid ceramide deacylase.
XX
SQ Sequence 954 AA:

Query Match 42.2%; Score 43; DB 23; Length 954;
Best Local Similarity 34.8%; Pred. NO. 1.5e+02;
Matches 8; Conservative 4; Mismatches 5; Indels 6; Gaps 1;

QY 2 TSSZPCGAVMILYFH-----KWR 18
: :|| :||| :||
Db 929 SCEOAGAAALILYHNHDSNQKWK 951

RESULT 7
AAU78470
ID AAU78470 standard; Protein; 992 AA.
XX
AC AAU78470;
XX
DT 02-JUL-2002 (first entry)
XX
DE Sphingolipid ceramide deacylase #2.
XX
DE Sphingolipid ceramide deacylase; nootropic; neuroprotective; cyrostatic;
XX
KW vulnerary; neurodegenerative disease; leukaemia; wound; enzyme.
XX
OS Shewanella alga.
XX
PN WO200226963-A1.
XX
PD 04-APR-2002.
XX
PF 26-SEP-2001; 2001WO-JP08344.
XX
PR 26-SEP-2000; 2000JP-0293181.
XX
PA (TAKI) TAKARA SHUZO CO LTD.
XX
PI Ito M, Furusato M, Sueyoshi N;
XX
XX WPI; 2002-340011/37.
DR N-PSDB; ABK47651.
XX
PT New polypeptide with sphingolipid ceramide deacylase activity and
PT encoded gene, applicable in studying structure and function of
PT sphingolipid and its engineering for treatment of e.g. neurodegenerative
PT neurodegenerative diseases and leukaemia -
XX
PS Example 2; Page 76-78; 89pp; Japanese.
XX
CC The invention relates to a polypeptide with sphingolipid ceramide
CC deacylase activity and its encoding nucleic acid. The polypeptide and its
CC encoded gene are applicable in studying structure and function of
CC sphingolipid and its engineering for treatment of e.g. neurodegenerative
CC diseases, leukaemia and wounds. The present sequence represents the
CC amino acid sequence of sphingolipid ceramide deacylase #2.
XX
SQ Sequence 992 AA:

Query Match 42.2%; Score 43; DB 23; Length 992;
Best Local Similarity 34.8%; Pred. NO. 1.6e+02;
Matches 8; Conservative 4; Mismatches 5; Indels 6; Gaps 1;

CC Down-regulation or out-competition of Mlo function may be used to
 CC stimulate a defence response in transgenic plants conferring increased
 CC pathogen resistance, especially resistance to powdery mildew or rust.
 CC The product can also be used for identifying compounds able to
 CC stimulate a defence response in a plant by interaction with
 CC encoded polypeptide.

XX Sequence 544 AA;

Query Match 40.2%; Score 41; DB 19; Length 544;
 Best Local Similarity 40.0%; Pred. No. 1.8e+02;
 Matches 10; Conservative 1; Mismatches 0; Indels 14; Gaps 1;

OY 8 AVML-----YFHKR 18
 |||||
 23 AVMLVSVAMEHALKLGHWFKMR 47

RESULT 13

AAU42094
 ID AAU42094 standard; Protein; 562 AA.

XX AAU42094;

DT 27-FEB-2002 (first entry)

XX Propionibacterium acnes immunogenic protein #2990.

XX SAPHO syndrome; synovitis; acne; pustulosis; hyperostosis; osteomyelitis;
 XX uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
 KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
 KW dermatological; osteopathic; neuroprotectant.

OS Propionibacterium acnes.

PN WO200101581-A2.

XX 01-NOV-2001.

PF 20-APR-2001; 2001WO-US12865.

PR 21-APR-2000; 2000US-199047P.

PR 02-JUN-2000; 2000US-208841P.

PR 07-JUL-2000; 2000US-216747P.

XX (CORI-) CORIXA CORP.

PI Skelly YAM, Persing DH, Mitcham JL, Wang SS, Bhatia A;
 PI L'maisonneuve J, Zhang Y, Jen S, Carter D;

DR N-PSDB; NMS59516.

PT Propionibacterium acnes polypeptides and nucleic acids useful for
 PT vaccinating against and diagnosing infections, especially useful for
 PT treating acne vulgaris.

XX Example 1; SEQ ID No 3289; 1069pp; English.

XX Sequences AAU9105-AAU68017 represent Propionibacterium acnes immunogenic
 CC polypeptides. The proteins and their associated DNA sequences are used in
 CC the treatment, prevention and diagnosis of medical conditions caused by
 CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
 CC pustulosis, hyperostosis and osteomyelitis), uveitis and endophthalmitis.
 CC P. acnes is also involved in infections of bone, joints and the central
 CC nervous system, however it is particularly involved in the inflammatory
 CC lesions associated with acne vulgaris. A method for detecting the
 CC presence or absence of P. acnes in a patient comprises contacting a
 CC sample with a binding agent that binds to the proteins of the invention
 CC and determining the amount of bound protein in the sample. The
 CC polypeptides may be used as antigens in the production of antibodies
 CC specific for P. acnes proteins. These antibodies can be used to
 CC downregulate expression and activity of P. acnes polypeptides and

CC therefore treat P. acnes infections. The antibodies may also be used as
 CC diagnostic agents for determining P. acnes presence, for example, by
 CC enzyme linked immunosorbent assay (ELISA).
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 562 AA;

Query Match 40.2%; Score 41; DB 22; Length 562;
 Best Local Similarity 31.8%; Pred. No. 1.9e+02;
 Matches 7; Conservative 4; Mismatches 5; Indels 6; Gaps 1;

OY 2 TS2PCGAVMI-----LYFHKW 17
 |||||
 23 THGPAGAILVCCIFKAMVHHSW 44

RESULT 14

ABBA8756
 ID ABBA8756 standard; Protein; 575 AA.

XX ABBA8756;

DT 05-FEB-2002 (first entry)

XX Listeria monocytogenes protein #1460.

XX Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation;
 KW vitamin B12; bacterial infection; disease.

OS Listeria monocytogenes.

PN WO200177335-A2.

XX 18-OCT-2001.

PF 11-APR-2001; 2001WO-FR01118.

PR 11-APR-2000; 2000FR-0004629.

XX (INSP) INST PASTEUR.

PI Buchrieser C, Frangeul L, Couve E, Rusniok C, Esli H, Dehoux P;
 PI Dussurget O, Chetouani F, Nedjari H, Glaser P, Kunst F, Cossart P;
 PI Daniels J, Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA;

PI Dominguez-Bernal G, Garrido-Garcia P, Tlherrez-Martinez A, Amend A;
 PI Chakraborty T, Bernal E, Hain T, Berche P, Chardit A, Durant L;
 PI Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N;

PI Madueno E, De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J;
 PI Rose M, Voss H;

DR WPI; 2002-010914/01.

PT Genomic sequence for Listeria monocytogenes, useful e.g. for treatment
 PT and prevention of Listeria and related bacterial infections, and
 PT related polypeptides.

XX Claim 6; SEQ ID No 1461; 192pp; French.

XX The present invention relates to the genome sequence of Listeria
 CC monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of
 CC it are useful for selecting probes and primers for detecting genes in L.
 CC monocytogenes and related organisms, and for studying genetic
 CC polymorphisms and other genomes. The present sequence is a protein
 CC encoded by the genome sequence of the present invention. Proteins
 CC expressed from the genome sequence are useful for raising specific
 CC antibodies. Identification of L. monocytogenes and related organisms, and
 CC for biosynthesis and biodegradation, especially biosynthesis of Vitamin
 CC B12. The genome sequence and proteins encoded by it are also useful for
 CC selecting compounds that regulate gene expression and cell replication
 CC and modulate L. monocytogenes-related diseases. In addition, the genome
 CC sequence and proteins encoded by it are useful in pharmaceutical and

CC vaccine compositions for the treatment or prevention of infections by L.
CC monocytoenes and related organisms.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at [ftp.wipo.int/pub/published_pat_sequences](http://wipo.int/pub/published_pat_sequences).

50 Sequence 575 AA;

every Match	40.28;	Score 41;	DB 23;	Length 575;
at Local similarity	50.0%;	Prod No 1	9c103.	

Best Local Similarity 50.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 7 GAVMILYFHKWR 18

```

Db      150 GAIILFFMDWK 161
          ||::||:| |:

```

RESULT 15

ID	AA	Y08613	standard; Protein; 60 AA.
1	AA	Y08613	standard; Protein; 60 AA.

AC AAY08613;

05-AUG-1999 (first entry)

DE Inter-alpha-trypsin inhibitor (BPI type) protein fragment TIBOR.

KW APP; beta-amyloid precursor protein; human; transgenic mice; pathology; Alzheimer's disease; therapeutic compounds; beta-amyloid; amyloid plaques

KW nerve tissue specific promoter; synthesis; inhibitor; deposition; plaque formation; treatment

XX	OS	Identified

XX
PN
HS5912410-A

XX 15-JUN-1999

XX 13-APR-1995
PF

XX 21-OCT-1994; 94US-0327381.
PR

PR	13-JUN-1990;	90US-0538857
PR	17-JUN-1991;	91US-0716725

PR 13-APR-1995; 9505-04623333-
XX

PA (SC10-) SCIOS INC.
XX

P1 Cordell B;
XX

DR WFL; 1999-35/231/30.
XX

transgenic mice useful for the treatment of Alzheimer's

PS Disclosure; Flq 8B; 72pp; Er

CC This invention describes now

related to the pathology of
for studying potentially the

CC contain a DNA sequence enriched
CC and a nerve tissue specific

Query Match	39.2%	Score 40;	DB 20;	Length 60;
Best Local Similarity	63.6%	Pred. No. 26;		
Matches	7;	Conservative	1;	Mismatches 3; Indels 0; Gaps 0

5 PCGAVMILYFH 15

Db 15 PCKAMIRYFY 25

Search completed: November 15, 2002, 11:44:12
Job time : 36 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 15, 2002, 11:43:15 ; Search time 14 Seconds
(without alignments)
37.829 Million cell updates/sec

Title: US-09-881-569A-2

Perfect score: 102

Sequence: 1 BTSPCGAMILYFHKWR 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 segs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Minimum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCFUS.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/Backfile1.pep:*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	39.2	60	1	US-08-358-160-112
2	40	39.2	60	6	US-08-422-333-14
3	40	39.2	60	6	5187153-22
4	40	39.2	60	6	5220013-25
5	40	39.2	60	6	5223482-24
6	40	39.2	60	6	5466783-5
7	40	39.2	476	4	US-09-632-021-2
8	39	38.2	111	1	US-08-084-718-61
9	39	38.2	111	1	US-08-443-976-61
10	39	38.2	111	1	US-08-443-977-61
11	39	38.2	504	4	US-09-499-302A-9
12	38	37.3	69	1	US-08-358-160-115
13	37.5	36.8	346	4	US-09-134-001C-5196
14	37	36.3	58	1	US-08-358-160-110
15	37	36.3	59	1	US-08-358-160-111
16	37	36.3	323	4	US-08-878-474-7
17	37	36.3	325	4	US-08-878-474-9
18	37	36.3	394	4	US-08-791-115B-27
19	37	36.3	403	4	US-08-791-115B-11
20	37	36.3	403	4	US-08-791-115B-23
21	37	36.3	403	4	US-08-791-115B-25
22	37	36.3	430	4	US-08-791-115B-7
23	37	36.3	536	2	US-08-484-993B-4
24	37	36.3	536	2	US-08-484-158B-4
25	37	36.3	536	2	US-08-484-158B-4
26	37	36.3	536	2	US-08-480-150A-4
27	37	36.3	536	3	US-08-458-731-4

28	37	36.3	536	3	US-08-149-222A-4	Sequence 4, Appl1
29	37	36.3	565	4	US-08-906-156A-12	Sequence 12, Appl1
30	37	36.3	645	4	US-08-791-115B-6	Sequence 6, Appl1
31	37	36.3	742	4	US-08-791-115B-5	Sequence 5, Appl1
32	37	36.3	900	4	US-08-890-865A-4	Sequence 4, Appl1
33	36.5	35.8	238	4	US-08-944-483-39	Sequence 39, Appl1
34	36.5	35.8	262	1	US-08-744-026-4	Sequence 4, Appl1
35	36.5	35.8	262	2	US-08-790-137-1	Sequence 1, Appl1
36	36.5	35.8	262	2	US-08-790-137-3	Sequence 3, Appl1
37	36.5	35.8	262	2	US-08-681-151-4	Sequence 4, Appl1
38	36.5	35.8	262	2	US-09-102-732-4	Sequence 4, Appl1
39	36.5	35.8	262	2	US-08-824-874-4	Sequence 4, Appl1
40	36.5	35.8	262	3	US-08-807-151-4	Sequence 4, Appl1
41	36.5	35.8	262	4	US-09-261-767-4	Sequence 4, Appl1
42	36.5	35.8	262	4	US-09-210-084-4	Sequence 4, Appl1
43	36.5	35.8	262	4	US-09-478-957-4	Sequence 4, Appl1
44	36	35.3	15	1	US-07-598-737C-17	Sequence 17, Appl1
45	36	35.3	19	4	US-08-974-549A-118	Sequence 118, App

ALIGNMENTS

RESULT 1
US-08-358-160-112
Sequence 112, Application US/08358160
Patent No. 5663143
GENERAL INFORMATION:
APPLICANT: LEY, Arthur C.
APPLICANT: LADNER, Robert C.
APPLICANT: GUTERMAN, Sonia K.
APPLICANT: ROBERTS, Bruce L.
APPLICANT: MARKLAND, William
APPLICANT: KENT, Rachel B.
TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
NUMBER OF SEQUENCES: 234
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEWMARK
STREET: 419 Seventh Street, N.W. Suite 300
CITY: Washington
STATE: District of Columbia
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/358,160
FILING DATE: 16-DEC-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,031
FILING DATE: 13-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,319
FILING DATE: 26-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/664,989
FILING DATE: 01-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/487,063
FILING DATE: 02-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/240,160
FILING DATE: 02-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Cooper, Iver P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: LEY-1
TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
LENGTH: 60 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-358-160-112

Query Match 39.2%; Score 40; DB 1; Length 60;
Best Local Similarity 63.6%; Pred. No. 35;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

5 PCGAVMILYFH 15
||| |||
DB 15 PCKAAMIRYFY 25

RESULT 2
US-08-422-333-14
Sequence 14, Application US/08422333
Patent No. 5912410

GENERAL INFORMATION:
APPLICANT: CORDELL, Barbara L.
TITLE OF INVENTION: TRANSGENIC NON-HUMAN MAMMAL DISPLAYING
TITLE OF INVENTION: THE AMYLOID-FORMING PATHOLOGY OF ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scios, Inc.
STREET: 2450 Bayshore Parkway
CITY: Mountain View
STATE: CA
COUNTRY: USA
ZIP: 94043

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/422.333
FILING DATE: 13-APR-1995
CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:
NAME: Shearer, Peter R.
REGISTRATION NUMBER: 28,117
REFERENCE/DOCKET NUMBER: 21900-28048.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 966-1550
TELEFAX: (415) 968-2438
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 60 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-422-333-14

Query Match 39.2%; Score 40; DB 2; Length 60;
Best Local Similarity 63.6%; Pred. No. 35;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

5 PCGAVMILYFH 15
||| |||
DB 15 PCKAAMIRYFY 25

RESULT 3
5187153-22
Patent No. 5187153

APPLICANT: CORDELL, BARBARA; SCHILLING, JAMES W.; KATUNUMA, NOBUHIKO
TITLE OF INVENTION: METHODS OF TREATMENT USING ALZHEIMER'S
AMYLOID POLYPEPTIDE DERIVATIVES
NUMBER OF SEQUENCES: 33
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/502,273
FILING DATE: 29-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 361,912
FILING DATE: 06-JUN-1989
APPLICATION NUMBER: 359,911
FILING DATE: 12-MAY-1989
APPLICATION NUMBER: 87,002
FILING DATE: 18-AUG-1987
APPLICATION NUMBER: 8,810
FILING DATE: 30-JAN-1987
APPLICATION NUMBER: 948,376
FILING DATE: 31-DEC-1986
APPLICATION NUMBER: 932,193
FILING DATE: 17-NOV-1986
SEQ ID NO: 22
LENGTH: 60
5187153-22

Query Match 39.2%; Score 40; DB 6; Length 60;
Best Local Similarity 63.6%; Pred. No. 35;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

5 PCGAVMILYFH 15
||| |||
DB 15 PCKAAMIRYFY 25

RESULT 4
5220013-25
Patent No. 5220013
APPLICANT: PONTE, PHYLLIS A.; CORDELL, BARBARA
TITLE OF INVENTION: DNA SEQUENCE USEFUL FOR THE DETECTION
OF ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/444,118
FILING DATE: 30-NOV-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 87,002
FILING DATE: 18-AUG-1987
APPLICATION NUMBER: 8,810
FILING DATE: 30-JAN-1987
APPLICATION NUMBER: 948,376
FILING DATE: 31-DEC-1986
APPLICATION NUMBER: 932,193
FILING DATE: 17-NOV-1986
SEQ ID NO: 25
LENGTH: 60
5220013-25

Query Match 39.2%; Score 40; DB 6; Length 60;
Best Local Similarity 63.6%; Pred. No. 35;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

5 PCGAVMILYFH 15
||| |||
DB 15 PCKAAMIRYFY 25

RESULT 5
5223482-24
Patent No. 5223482
APPLICANT: SCHILLING, JAMES W.; PONTE, PHYLLIS A.; CORDELL,
BARBARA
TITLE OF INVENTION: RECOMBINANT ALZHEIMER'S PROTEINASE
INHIBITORY AMYLOID PROTEIN AND METHOD OF USE
NUMBER OF SEQUENCES: 34


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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/361,912
; FILING DATE: 06-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 359,911
; FILING DATE: 12-MAY-1989
; APPLICATION NUMBER: 87,002
; FILING DATE: 18-AUG-1987
; APPLICATION NUMBER: 8,810
; FILING DATE: 30-JAN-1987
; APPLICATION NUMBER: 948,376
; FILING DATE: 31-DEC-1986
; APPLICATION NUMBER: 932,193
; FILING DATE: 17-NOV-1986
; SEQ ID NO:24
; LENGTH: 60
5223482-24
;
Query Match      39.28; Score 40; DB 6; Length 60;
Best Local Similarity 63.68; Pred. No. 35;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      5 PCGAVMILYFH 15
      ||| |||
      15 PCKAMIRYFY 25

RESULT 6
546783-5
; Patent No. 546783
; APPLICANT: Mun, Tze-Cheln; Kretzmer, Kuniko K.; Broze,
; George J. Jr.
; TITLE OF INVENTION: HUMAN TISSUE FACTOR INHIBITOR
; NUMBER OF SEQUENCES: 26
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/93,285
; FILING DATE: 15-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 566,280
; FILING DATE: 13-AUG-1990
; APPLICATION NUMBER: 123,753
; FILING DATE: 23-NOV-1987
; APPLICATION NUMBER: 77,366
; FILING DATE: 23-JUL-1987
; SEQ ID NO:5;
; LENGTH: 60
546783-5

Query Match      39.28; Score 40; DB 6; Length 60;
Best Local Similarity 63.68; Pred. No. 35;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

      5 PCGAVMILYFH 15
      ||| |||
      15 PCKAMIRYFY 25

DB      15 PCKAMIRYFY 25

RESULT 7
US-09-632-021-2
; Sequence 2, Application US/09632021
; Patent No. 6406896
; GENERAL INFORMATION:
; APPLICANT: Reznikoff, William S
; APPLICANT: Naumann, Todd A
; TITLE OF INVENTION: Transposase Enzyme and Method for Use
; FILE REFERENCE: 960296.96471
; CURRENT APPLICATION NUMBER: US/09/632,021
; CURRENT FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/146686
; PRIOR FILING DATE: 1999-08-02
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
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; LENGTH: 476
; TYPE: PRF
; ORGANISM: Transposon Tn5
US-09-632-021-2

Query Match      39.28; Score 40; DB 4; Length 476;
Best Local Similarity 34.88; Pred. No. 2,2e-02;
Matches 8; Conservative 5; Mismatches 4; Indels 6; Gaps 1;

QY      2 TSZPCGA-----VMILYFHKWR 18
      ||| | : | : | : | : |
      302 TSEPVESLAQALRVIDYTHRMW 324

DB      302 TSEPVESLAQALRVIDYTHRMW 324

RESULT 8
US-08-084-718-61
; Sequence 61, Application US/08084718
; Patent No. 5591603
; GENERAL INFORMATION:
; APPLICANT: Bjorn, Soeren E.
; APPLICANT: No. 5591603ris, Kjeld
; APPLICANT: Dines, Vigeo
; APPLICANT: No. 5591603rskov-Lauritsen, Lelf
; APPLICANT: Christensen, Niels D.
; APPLICANT: Bregengaard, Claus
; APPLICANT: No. 5591603ris, Fanny
; APPLICANT: Petersen, Lars C.
; TITLE OF INVENTION: Process for the Preparation of Aprotinin
; NUMBER OF SEQUENCES: 83
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 55916030 No. 5591603disk of NO. 5591603th America, Inc.
; STREET: 405 Lexington Avenue, 62nd Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/084,718
; FILING DATE: 19930623
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 4501/87
; FILING DATE: 28-AUG-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 2254/88
; FILING DATE: 26-APR-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/DK88/00138
; FILING DATE: 28-AUG-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/DK89/00096
; FILING DATE: 25-APR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/466,408
; FILING DATE: 21-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 2361/90
; FILING DATE: 01-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/598,337
; FILING DATE: 19-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 1118/91
; FILING DATE: 12-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/DK91/00299
; FILING DATE: 01-OCT-1991
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,687
FILING DATE: 29-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/024,925
FILING DATE: 26-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: Agriis, Cheryl H.
REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 3143.224-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-867-0298
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-084-718-61

Query Match 38.2%; Score 39; DB 1; Length 111;
Best Local Similarity 63.6%; Pred. NO. 84;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 PCGAVMILYFH 15
|||:||||:
DB 66 PCKARILLYFY 76

RESULT 9
US-08-443-976-61
Sequence 61, Application US/08443976
Patent No. 5618915
GENERAL INFORMATION:
APPLICANT: Bjorn, Soeren E.
APPLICANT: No. 5618915r1s, Kjeld
APPLICANT: Diness, V1990
APPLICANT: No. 5618915rskov-Lauritsen, Lelf
APPLICANT: Christensen, Niels D.
APPLICANT: Bregengaard, Claus
APPLICANT: No. 5618915r1s, Fanny
APPLICANT: Petersen, Lars C.
TITLE OF INVENTION: Process for the Preparation of Aprotinin
TITLE OF INVENTION: and Aprotinin Analogs
NUMBER OF SEQUENCES: 83
CORRESPONDENCE ADDRESSES:
ADDRESSEE: No. 5618915d1sk of No. 5618915th America, Inc.
STREET: 405 Lexington Avenue, 62nd Floor
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/443,976
FILING DATE: 18-MAY-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/084,718
FILING DATE: 23-JUN-1993
APPLICATION NUMBER: DK 4501/87
FILING DATE: 28-AUG-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 2254/88
FILING DATE: 26-APR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DK88/00138
FILING DATE: 28-AUG-1988

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DK89/00096
FILING DATE: 25-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/466,408
FILING DATE: 21-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 2361/90
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/598,337
FILING DATE: 19-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 1118/91
FILING DATE: 12-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DK91/00299
FILING DATE: 01-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,687
FILING DATE: 29-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/024,925
FILING DATE: 26-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: Agriis, Cheryl H.
REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 3143.224-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-867-0298
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-443-976-61

Query Match 38.2%; Score 39; DB 1; Length 111;
Best Local Similarity 63.6%; Pred. NO. 84;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 PCGAVMILYFH 15
|||:||||:
DB 66 PCKARILLYFY 76

RESULT 10
US-08-443-977-61
Sequence 61, Application US/08443977
Patent No. 5621074
GENERAL INFORMATION:
APPLICANT: Bjorn, Soeren E.
APPLICANT: No. 5621074r1s, Kjeld
APPLICANT: Diness, V1990
APPLICANT: No. 5621074rskov-Lauritsen, Lelf
APPLICANT: Christensen, Niels D.
APPLICANT: Bregengaard, Claus
APPLICANT: No. 5621074r1s, Fanny
APPLICANT: Petersen, Lars C.
TITLE OF INVENTION: Process for the Preparation of Aprotinin
TITLE OF INVENTION: and Aprotinin Analogs
NUMBER OF SEQUENCES: 83
CORRESPONDENCE ADDRESSES:
ADDRESSEE: No. 5621074d1sk of No. 5621074th America, Inc.
STREET: 405 Lexington Avenue, 62nd Floor
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/443,977
FILING DATE: 18-MAY-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/084,718
FILING DATE: 23-JUN-1993
APPLICATION NUMBER: DK 4501/87
FILING DATE: 28-AUG-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 2254/88
FILING DATE: 26-APR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DK88/00138
FILING DATE: 28-AUG-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DK89/00096
FILING DATE: 25-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/466,408
FILING DATE: 21-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 2361/90
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/598,337
FILING DATE: 19-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 1118/91
FILING DATE: 12-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DK91/00299
FILING DATE: 01-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,687
FILING DATE: 29-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/024,925
FILING DATE: 26-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: Agtis, Cheryl H.
REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 3143,224-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-867-0298
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-443-977-61

Query Match 38.2% Score 39; DB 1; Length 111;
Best Local Similarity 63.6% Pred. No. 84;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 PCGAWILYFH 15
|||:||||:
DB 66 PCKARILLYF 76

RESULT 11
US-09-499-302a-9
Sequence 9, Application US/09499302A
Patent No. 6369212
GENERAL INFORMATION:
SOFTWARE: BOUNG-JUN, OH
APPLICANT: MOON, KYUNG KO

APPLICANT: YOUNG, SOON KIM
TITLE OF INVENTION: A CYTOCHROME P450 GENE HIGHLY EXPRESSED IN THE
TITLE OF INVENTION: INCOMPATIBLE INTERACTION
FILE REFERENCE: 10324/P64443USO
CURRENT APPLICATION NUMBER: US/09/499,302A
CURRENT FILING DATE: 2000-02-07
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 9
LENGTH: 504
TYPE: PR1
ORGANISM: Arabidopsis sp.
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (1)
OTHER INFORMATION: variable or unknown amino acid
NAME/KEY: MOD_RES
LOCATION: (62)
OTHER INFORMATION: variable or unknown amino acid
NAME/KEY: MOD_RES
LOCATION: (243)
OTHER INFORMATION: variable or unknown amino acid
NAME/KEY: MOD_RES
LOCATION: (246)
OTHER INFORMATION: variable or unknown amino acid
NAME/KEY: MOD_RES
LOCATION: (253)
OTHER INFORMATION: variable or unknown amino acid
NAME/KEY: MOD_RES
LOCATION: (324)
OTHER INFORMATION: variable or unknown amino acid
NAME/KEY: MOD_RES
LOCATION: (394)
OTHER INFORMATION: variable or unknown amino acid
US-09-499-302a-9

Query Match 38.2% Score 39; DB 4; Length 504;
Best Local Similarity 54.5% Pred. No. 3,2e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 7 GAWMILYFHKW 17
|:|||||:
DB 459 GLMLLYFFDW 469

RESULT 12
US-08-358-160-115
Sequence 115, Application US/08358160
Patent No. 5663143
GENERAL INFORMATION:
APPLICANT: LEY, Arthur C.
APPLICANT: LADNER, Robert C.
APPLICANT: GUTERMAN, Sonia K.
APPLICANT: ROBERTS, Bruce L.
APPLICANT: MARKLAND, William
APPLICANT: KENT, Rachel B.
TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
NUMBER OF SEQUENCES: 234
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W. Suite 300
CITY: Washington
STATE: District of Columbia
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/358,160

FILING DATE: 16-DEC-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,031
FILING DATE: 13-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,319
FILING DATE: 26-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/664,989
FILING DATE: 01-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/487,063
FILING DATE: 02-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/240,160
FILING DATE: 02-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Cooper, Iver P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: LEY-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 115:
SEQUENCE CHARACTERISTICS:
LENGTH: 69 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-358-160-115

Query Match 37.3%; Score 38; DB 1; Length 69;
Best Local Similarity 63.6%; Pred. No. 77;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 5 PCGAVMILYFPH 15
||| |||
Db 18 PCKAKMIRYFY 28

RESULT 13
US-09-134-001C-5196
Sequence 5196, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 5196
LENGTH: 346
TYPE: PRT
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5196

Query Match 36.8%; Score 37.5; DB 4; Length 346;
Best Local Similarity 43.8%; Pred. No. 3,7e+02;
Matches 7; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

OY 3 SZPCGAVMILYFHK-W 17
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Db 129 SIPLGIIMAVYHKIM 144

RESULT 14
US-08-358-160-110
Sequence 110, Application US/08358160
Patent No. 5663143
GENERAL INFORMATION:
APPLICANT: LEY, Arthur C.
APPLICANT: LADNER, Robert C.
APPLICANT: GUTERMAN, Soula K.
APPLICANT: ROBERTS, Bruce L.
APPLICANT: MARKLAND, William

APPLICANT: KENT, Rachel B.
TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
NUMBER OF SEQUENCES: 234
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W. Suite 300
CITY: Washington
STATE: District of Columbia
COUNTRY: USA
ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/358,160
FILING DATE: 16-DEC-1994
CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,031
FILING DATE: 13-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,319
FILING DATE: 26-JAN-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/664,989
FILING DATE: 01-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/487,063
FILING DATE: 02-MAR-1990

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/240,160
FILING DATE: 02-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Cooper, Iver P.

REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: LEY-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633

INFORMATION FOR SEQ ID NO: 110:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-358-160-110

Query Match 36.3%; Score 37; DB 1; Length 58;
Best Local Similarity 63.6%; Pred. No. 91;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 5 PCGAVMILYFPH 15
||| |||
Db 13 PCKAKMIRYFY 23

RESULT 15

US-08-358-160-111
 ; Sequence 111, Application US/08358160
 ; Patent No. 5663143
 ; GENERAL INFORMATION:
 ; APPLICANT: LEY, Arthur C.
 ; APPLICANT: LADNER, Robert C.
 ; APPLICANT: GUTERMAN, Sonia K.
 ; APPLICANT: ROBERTS, Bruce L.
 ; APPLICANT: MARKLAND, William
 ; APPLICANT: KENT, Rachel B.
 ; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
 ; DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
 ; NUMBER OF SEQUENCES: 234
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: BROWDY AND NEIMARK
 ; STREET: 419 Seventh Street, N.W. Suite 300
 ; CITY: Washington
 ; STATE: District of Columbia
 ; COUNTRY: USA
 ; ZIP: 20004
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/358,160
 ; FILING DATE: 16-DEC-1994
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/133,031
 ; FILING DATE: 13-OCT-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/009,319
 ; FILING DATE: 26-JAN-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/664,989
 ; FILING DATE: 01-MAR-1991
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/487,063
 ; FILING DATE: 02-MAR-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/240,160
 ; FILING DATE: 02-SEP-1988
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Cooper, Iver P.
 ; REGISTRATION NUMBER: 28,005
 ; REFERENCE/DOCKET NUMBER: LEY-1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-628-5197
 ; TELEFAX: 202-737-3528
 ; TELEX: 248633
 ; INFORMATION FOR SEQ ID NO: 111:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 59 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-358-160-111

Query Match 36.3%; Score 37; DB 1; Length 59;
 Best Local Similarity 63.6%; Pred. No. 92;
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 PCGAVMILYFH 15
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 DB 14 PCKAKMIRIFY 24

Search completed: November 15, 2002, 11:45:31
 Job time : 15 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 15, 2002, 11:44:39 ; Search time 10 Seconds
(without alignments)
27.110 Million cell updates/sec

Title: US-09-881-569A-2

Perfect score: 102

Sequence: 1 BTSPCGAVMILYFHKWR 18

Scoring table: BLOSUM62

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Searched: 97044 seqs, 15060890 residues

Total number of hits satisfying chosen parameters: 97044

Minimum DB seq length: 0

Minimum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications, AA.*

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- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
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- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
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- 12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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3	44	43.1	893	10	US-09-906-453-4
4	39	38.2	39	10	US-09-864-761-48038
5	38	37.3	74	10	US-09-764-870-484
6	38	37.3	1185	9	US-09-895-913A-246
7	38	37.3	1185	10	US-09-815-242-11466
8	37	36.3	111	10	US-09-864-761-37111
9	37	36.3	318	12	US-10-028-051-8
10	37	36.3	323	9	US-09-903-170C-7
11	37	36.3	323	10	US-09-903-180B-7
12	37	36.3	323	10	US-09-903-180B-7
13	37	36.3	323	10	US-09-903-171A-7
14	37	36.3	323	10	US-09-903-188A-7
15	37	36.3	323	10	US-09-903-323A-7
16	37	36.3	323	10	US-09-903-325A-7
17	37	36.3	325	9	US-09-903-170C-9
18	37	36.3	325	9	US-09-974-298-17
19	37	36.3	325	10	US-09-903-180B-9

20	37	36.3	325	10	US-09-903-187A-9	Sequence 9, Appl 1
21	37	36.3	325	10	US-09-903-171A-9	Sequence 9, Appl 1
22	37	36.3	325	10	US-09-903-188A-9	Sequence 9, Appl 1
23	37	36.3	325	10	US-09-903-323A-9	Sequence 9, Appl 1
24	37	36.3	325	10	US-09-903-325A-9	Sequence 9, Appl 1
25	37	36.3	325	12	US-10-028-051-2	Sequence 2, Appl 1
26	37	36.3	325	12	US-10-028-051-4	Sequence 2, Appl 1
27	37	36.3	403	10	US-09-870-379-2	Sequence 2, Appl 1
28	37	36.3	71	12	US-10-001-879-194	Sequence 194, App
29	36.5	35.8	262	10	US-09-796-294-9	Sequence 9, Appl 1
30	36.5	35.8	262	10	US-09-764-762-4	Sequence 4, Appl 1
31	36.5	35.8	262	10	US-09-988-975A-7	Sequence 7, Appl 1
32	36.5	35.8	267	10	US-09-925-297-745	Sequence 745, App
33	36	35.3	28	10	US-09-864-761-44551	Sequence 44551, A
34	36	35.3	49	10	US-09-764-887-204	Sequence 204, App
35	36	35.3	57	8	US-08-896-322-5	Sequence 5, Appl 1
36	36	35.3	276	10	US-09-925-300-1624	Sequence 1624, Ap
37	36	35.3	552	9	US-09-843-676-4	Sequence 4, Appl 1
38	36	35.3	839	10	US-09-768-877-25	Sequence 25, Appl 1
39	36	35.3	842	10	US-09-798-831-8	Sequence 8, Appl 1
40	36	35.3	891	10	US-09-949-192-45	Sequence 45, Appl 1
41	36	35.3	1356	10	US-09-801-368-306	Sequence 306, App
42	35	34.3	38	10	US-09-864-761-44559	Sequence 44559, A
43	35	34.3	66	10	US-09-764-877-1085	Sequence 1085, Ap
44	35	34.3	136	10	US-09-970-711-5	Sequence 5, Appl 1
45	35	34.3	160	10	US-09-731-872-316	Sequence 316, App

ALIGNMENTS

RESULT 1
US-09-881-569A-2
; Sequence 2, Application US/09881569A
; Patent No. US20020151687A1
; GENERAL INFORMATION:
; APPLICANT: KHANNA, PUSHA
; TITLE OF INVENTION: PROTEIN/POLYPEPTIDE-K OBTAINED FROM MOMORDICA CHARANTIA
; TITLE OF INVENTION: AND A PROCESS FOR THE EXTRACTION THEREOF
; FILE REFERENCE: 013488-3
; CURRENT APPLICATION NUMBER: US/09/881,569A
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 560/DEL/99
; PRIOR FILING DATE: 1999-04-13
; PRIOR APPLICATION NUMBER: 561/DEL/99
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Polypeptide-K
; OTHER INFORMATION: Isolated from momordica charantia
US-09-881-569A-2

Query Match 100.0%; Score 102; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.4e-10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 BTSPCGAVMILYFHKWR 18
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Db 1 BTSPCGAVMILYFHKWR 18

RESULT 2
US-09-881-569A-1
; Sequence 1, Application US/09881569A
; Patent No. US20020151687A1
; GENERAL INFORMATION:
; APPLICANT: KHANNA, PUSHA
; TITLE OF INVENTION: PROTEIN/POLYPEPTIDE-K OBTAINED FROM MOMORDICA CHARANTIA

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; TITLE OF INVENTION: AND A PROCESS FOR THE EXTRACTION THEREOF
; FILE REFERENCE: 013488-3
; CURRENT APPLICATION NUMBER: US/09/881,569A
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 560/DEL/99
; PRIOR FILING DATE: 1999-04-13
; PRIOR APPLICATION NUMBER: 561/DEL/99
; PRIOR FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 1
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Polypeptide-p
-09-881-569A-1

Query Match
Best Local Similarity 57.8%; Score 59; DB 10; Length 16;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 BRTSPCGAVMILYFHKR 16
DB 1 DTSEPGAVCMILYFHKR 16

RESULT 3
US-09-906-453-4
; Sequence 4, Application US/09906453
; Patent No. US20020120125A1
; GENERAL INFORMATION:
; APPLICANT: Kaeppler, Shawn
; APPLICANT: Springer, Nathan
; APPLICANT: Helentjaris, Timothy
; APPLICANT: Phillips, Ronald
; TITLE OF INVENTION: Polycarb genes from Maize - Mez1 and Mez2
; FILE REFERENCE: WISCONSIN10005
; CURRENT APPLICATION NUMBER: US/09/906,453
; CURRENT FILING DATE: 2001-07-16
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 4
; LENGTH: 893
; TYPE: PRT
; ORGANISM: Zea mays
US-09-906-453-4

Query Match
Best Local Similarity 43.1%; Score 44; DB 10; Length 893;
Matches 7; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 BRTSPCGAVMILYFHKR 18
DB 317 ENKKGCHLCYLRFPQNR 334

RESULT 4
US-09-864-761-48038
; Sequence 48038, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecm1ca-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
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; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO: 48038
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC009966.2
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.9
US-09-864-761-48038

Query Match
Best Local Similarity 38.2%; Score 39; DB 10; Length 39;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 3 SZPCGAVMILYFHKW 17
DB 21 SEPTGLEMIHYSYLW 35

RESULT 5
US-09-764-870-484
; Sequence 484, Application US/09764870
; Patent No. US20020042386A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT214
; CURRENT APPLICATION NUMBER: US/09/764,870
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 646
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 484
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-870-484
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, RESULT 7
US-09-815-242-11466
, Sequence 11466, Application US/09815242
, Patent No. US2002061569A1
, GENERAL INFORMATION:
, APPLICANT: Haselbeck, Robert
, APPLICANT: Ohlseen, Karl L.
, APPLICANT: Zyskind, Judith W.
, APPLICANT: Wall, Daniel
, APPLICANT: Trawick, John D.
, APPLICANT: Carr, Grant J.
, APPLICANT: Yamamoto, Robert T.
, APPLICANT: Xu, H. Howard
, TITLE OF INVENTION: Identification of Essential Genes in
, FILE REFERENCE: ELITRA.011A
, CURRENT APPLICATION NUMBER: US/09/815,242
, CURRENT FILING DATE: 2001-03-21
, PRIOR APPLICATION NUMBER: 60/191,078
, PRIOR FILING DATE: 2000-03-21
, PRIOR APPLICATION NUMBER: 60/206,848
, PRIOR FILING DATE: 2000-05-23
, PRIOR APPLICATION NUMBER: 60/207,727
, PRIOR FILING DATE: 2000-05-26
, PRIOR APPLICATION NUMBER: 60/242,578
, PRIOR FILING DATE: 2000-10-23
, PRIOR APPLICATION NUMBER: 60/253,625
, PRIOR FILING DATE: 2000-11-27

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1 PRIOR APPLICATION NUMBER: US 60/236,359
2 PRIOR FILING DATE: 2000-09-27
3 PRIOR APPLICATION NUMBER: PCT/US01/00666
4 PRIOR FILING DATE: 2001-01-30
5 PRIOR APPLICATION NUMBER: PCT/US01/00667
6 PRIOR FILING DATE: 2001-01-30
7 PRIOR APPLICATION NUMBER: PCT/US01/00664
8 PRIOR FILING DATE: 2001-01-30
9 PRIOR APPLICATION NUMBER: PCT/US01/00669
10 PRIOR FILING DATE: 2001-01-30
11 PRIOR APPLICATION NUMBER: PCT/US01/00665
12 PRIOR FILING DATE: 2001-01-30
13 PRIOR APPLICATION NUMBER: PCT/US01/00668
14 PRIOR FILING DATE: 2001-01-30
15 PRIOR APPLICATION NUMBER: PCT/US01/00663
16 PRIOR FILING DATE: 2001-01-30
17 PRIOR APPLICATION NUMBER: PCT/US01/00662
18 PRIOR FILING DATE: 2001-01-30
19 PRIOR APPLICATION NUMBER: PCT/US01/00661
20 PRIOR FILING DATE: 2001-01-30
21 PRIOR APPLICATION NUMBER: PCT/US01/00670
22 PRIOR FILING DATE: 2001-01-30
23 PRIOR APPLICATION NUMBER: US 60/234,687
24 PRIOR FILING DATE: 2000-09-21
25 PRIOR APPLICATION NUMBER: US 09/608,408
26 PRIOR FILING DATE: 2000-06-30
27 PRIOR APPLICATION NUMBER: US 09/774,203
28 PRIOR FILING DATE: 2001-01-29
29 NUMBER OF SEQ ID NOS: 49117
30 SOFTWARE: Anomax Sequence Listing Engine vers. 1.1.1

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SEQ ID NO 37111
LENGTH: 111
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AL023281.1
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 9.2
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 12
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 9.2
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 10
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 9.2
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 12
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 11
OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 10
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 16
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 13
OTHER INFORMATION: EST_HUMAN HIT: AW411290.1, EVALUE 5.00e-05
OTHER INFORMATION: SWISSPROT HIT: P81274, EVALUE 9.00e-06
US-09-864-761-37111

Query Match 36.3%; Score 37; DB 10; Length 111;
Best Local Similarity 42.9%; Pred. No. 31;
Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

OY 1 BRSZPCGAVMILYF 14
DB 85 DVAKTLGRVLLYF 98

RESULT 9

US-10-028-051-8
Sequence 8, Application US/10028051
Patent No. US20020147329A1
GENERAL INFORMATION:

APPLICANT: Luyten, Frank P.

Huang, Bang
Moos, Jr., Malcolm

Wang, Shouwen

TITLE OF INVENTION: ISOLATION AND USE OF TISSUE
GROWTH INDUCING FRZB PROTEIN

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSEE: Knobbe, Martens, Olson & Bear

STREET: 620 Newport Center Drive, 16th Floor

CITY: Newport Beach

STATE: CA

COUNTRY: U.S.A.

ZIP: 92660

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/028,051

FILING DATE: 19-Dec-2001

CLASSIFICATION: <unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/729,452

FILING DATE: <unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Bartfeld, Neil S

REGISTRATION NUMBER: 39,901

REFERENCE/DOCKET NUMBER: NIH133.001A

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619-235-8550

TELEFAX: 619-235-0176

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 318 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-028-051-8

Query Match 36.3%; Score 37; DB 12; Length 318;
Best Local Similarity 35.7%; Pred. No. 84;
Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

OY 4 ZPCGAVMILYFHKW 17
DB 114 QGCEPILIKYRHSW 127

RESULT 10

US-09-903-170C-7
Sequence 7, Application US/09903170C
Patent No. US20020156249A1
GENERAL INFORMATION:

APPLICANT: De Robertis, Edward M.

TITLE OF INVENTION: Endoderm, Cardiac and Neural Inducing

FILE REFERENCE: 510015-259

CURRENT APPLICATION NUMBER: US/09/903,170C

CURRENT FILING DATE: 2001-07-11

PRIOR APPLICATION NUMBER: US 60/020,150

PRIOR FILING DATE: 1996-06-20

NUMBER OF SEQ ID NOS: 10

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 7

LENGTH: 323

TYPE: PRT

ORGANISM: Mouse FRZB-1

US-09-903-170C-7

Query Match 36.3%; Score 37; DB 9; Length 323;
Best Local Similarity 35.7%; Pred. No. 85;
Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

OY 4 ZPCGAVMILYFHKW 17
DB 117 QGCEPILIKYRHSW 130

RESULT 11

US-09-903-180B-7
Sequence 7, Application US/09903180B
Patent No. US20020099171A1
GENERAL INFORMATION:

APPLICANT: De Robertis, Edward M.

TITLE OF INVENTION: Endoderm, Cardiac and Neural Inducing

FILE REFERENCE: 510015-256

CURRENT APPLICATION NUMBER: US/09/903,180B

CURRENT FILING DATE: 2001-07-11

PRIOR APPLICATION NUMBER: US 60/020,150

PRIOR FILING DATE: 1996-06-20

NUMBER OF SEQ ID NOS: 10

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 7

LENGTH: 323

TYPE: PRT

ORGANISM: Mouse FRZB-1

US-09-903-180B-7

Query Match 36.3%; Score 37; DB 10; Length 323;
Best Local Similarity 35.7%; Pred. No. 85;
Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

OY 4 ZPCGAVMILYFHKW 17
DB 117 QGCEPILIKYRHSW 130

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RESULT 12
US-09-903-187A-7
; Sequence 7, Application US/09903187A
; Patent No. US20020099172A1
; GENERAL INFORMATION:
; APPLICANT: De Robertis, Edward M.
; APPLICANT: Boumester, Lewis
; TITLE OF INVENTION: Endoderm, Cardiac and Neural Inducing
; TITLE OF INVENTION: Factors
; FILE REFERENCE: 510015-248
; CURRENT APPLICATION NUMBER: US/09/903,187A
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 09/552,988
; PRIOR FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: US 08/878,474
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: US 60/020,150
; PRIOR FILING DATE: 1996-06-20
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 323
; TYPE: PRT
; ORGANISM: Mouse

US-09-903-187A-7

Query Match          36.3%; Score 37; DB 10; Length 323;
Best Local Similarity 35.7%; Pred. No. 85;
Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 4 ZPCGAVMILYFHKW 17
; : : : : :
Db 117 QCCEPILIKYRHSW 130

RESULT 13
US-09-903-171A-7
; Sequence 7, Application US/09903171A
; Patent No. US20020123613A1
; GENERAL INFORMATION:
; APPLICANT: De Robertis, Edward M.
; APPLICANT: Boumester, Lewis
; TITLE OF INVENTION: Endoderm, Cardiac and Neural Inducing
; TITLE OF INVENTION: Factors
; FILE REFERENCE: 510015-260
; CURRENT APPLICATION NUMBER: US/09/903,171A
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: US 60/020,150
; PRIOR FILING DATE: 1996-06-20
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 323
; TYPE: PRT
; ORGANISM: Mouse FRZB-1

US-09-903-171A-7

Query Match          36.3%; Score 37; DB 10; Length 323;
Best Local Similarity 35.7%; Pred. No. 85;
Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 4 ZPCGAVMILYFHKW 17
; : : : : :
Db 117 QCCEPILIKYRHSW 130

RESULT 14
US-09-903-188A-7
; Sequence 7, Application US/09903188A
; Patent No. US20020128439A1
; GENERAL INFORMATION:
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; APPLICANT: De Robertis, Edward M.
; APPLICANT: Boumester, Lewis
; TITLE OF INVENTION: Endoderm, Cardiac and Neural Inducing
; TITLE OF INVENTION: Factors
; FILE REFERENCE: 510015-258
; CURRENT APPLICATION NUMBER: US/09/903,188A
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: US 60/020,150
; PRIOR FILING DATE: 1996-06-20
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 323
; TYPE: PRT
; ORGANISM: Mouse FRZB-1

US-09-903-188A-7

Query Match          36.3%; Score 37; DB 10; Length 323;
Best Local Similarity 35.7%; Pred. No. 85;
Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 4 ZPCGAVMILYFHKW 17
; : : : : :
Db 117 QCCEPILIKYRHSW 130

RESULT 15
US-09-903-323A-7
; Sequence 7, Application US/09903323A
; Patent No. US20020128440A1
; GENERAL INFORMATION:
; APPLICANT: De Robertis, Edward M.
; APPLICANT: Boumester, Lewis
; TITLE OF INVENTION: Endoderm, Cardiac and Neural Inducing
; TITLE OF INVENTION: Factors
; FILE REFERENCE: 510015-261
; CURRENT APPLICATION NUMBER: US/09/903,323A
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: US 60/020,150
; PRIOR FILING DATE: 1996-06-20
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 323
; TYPE: PRT
; ORGANISM: Mouse FRZB-1

US-09-903-323A-7

Query Match          36.3%; Score 37; DB 10; Length 323;
Best Local Similarity 35.7%; Pred. No. 85;
Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 4 ZPCGAVMILYFHKW 17
; : : : : :
Db 117 QCCEPILIKYRHSW 130
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Search completed: November 15, 2002, 11:48:26
Job time : 11 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 15, 2002, 11:43:14 ; Search time 15 Seconds

(without alignments)
115.361 Million cell updates/sec

Title: US-09-881-569A-2

Perfect score: 102

Sequence: 1 BRSZPCGAVMILYFHKMR 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Database :

1: PIR73:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Post-processing: Minimum Match 08
Maximum Match 100%
Listing first 45 summaries

SUMMARIES

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1	44	43.1	222	2 B69433	signal-transducing
2	44	43.1	758	2 A47439	gamma-glutamyl car
3	43	42.2	64	2 AC2277	hypothetical prote
4	43	42.2	1239	2 C71266	probable ATP-depen
5	42	41.2	221	2 D86600	SET domain protein
6	42	41.2	221	2 B81514	conserved hypotet
7	42	41.2	221	2 D72024	set domain protein
8	42	41.2	302	2 AE0958	probable lysR-fam
9	42	41.2	443	2 H83589	conserved hypotet
10	41	40.2	353	2 D84686	probable RAD51B-11
11	41	40.2	374	2 T09771	phosphatidate cycl
12	41	40.2	544	2 T05952	Mio-11 protein - b
13	41	40.2	558	2 T30418	chitinase (EC 3.2.
14	41	40.2	575	2 AB1793	ABC transporter (A
15	41	40.2	575	2 AH1417	ABC transporter (A
16	41	40.2	612	2 F83000	probable two-compo
17	41	40.2	623	2 D88922	protein W03P9.4 [1
18	40.5	39.7	2133	2 T10637	hypothetical prote
19	40	39.2	60	1 T10637	serum basic protei
20	40	39.2	100	2 S45888	hypothetical prote
21	40	39.2	195	2 AE3074	transcription regu
22	40	39.2	199	2 D98212	probable tetr-fam
23	40	39.2	272	2 T64245	hypothetical prote
24	40	39.2	536	2 T33480	hypothetical prote
25	40	39.2	590	2 A10094	ABC-transporter tr
26	40	39.2	830	1 A57060	serine/threonine-s
27	39.5	38.7	340	2 AE0353	probable membrane
28	39.5	38.7	737	1 JC5655	DnaMlp/Vpslp-like p
29	39.5	38.7	1010	2 T33572	hypothetical prote

30	39.5	38.7	1157	2 AD1358	ATP-dependent deox
31	39.5	38.7	1157	2 AD1728	ATP-dependent deox
32	39	38.2	148	2 D69541	flavodoxin homolog
33	39	38.2	284	2 H86898	undecaprenol kinas
34	39	38.2	328	2 F89914	hypothetical prote
35	39	38.2	388	1 WMLJBT	bel-2 protein - si
36	39	38.2	422	2 F70018	multiple sugar-bin
37	39	38.2	466	2 T24334	hypothetical prote
38	39	38.2	500	1 JE0259	cytochrome P450 2p
39	39	38.2	625	2 T41603	alpha-amylose - fl
40	39	38.2	738	2 C95936	conserved hypotet
41	39	38.2	860	2 C72338	hypothetical prote
42	39	38.2	1147	2 S64930	serine/threonine-s
43	38.5	37.7	75	2 A31298	alpha-amylose inh
44	38.5	37.7	227	2 I37019	cytochrome-c oxida
45	38.5	37.7	255	2 AF1556	conserved hypotet

ALIGNMENTS

RESULT 1

B69433 signal-transducing histidine kinase homolog - Archaeoglobus fulgidus

C:Species: Archaeoglobus fulgidus

C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 21-Jul-2000

C/Accession: B69433

R:Kienk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dod

Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Meldrum, J.E.; McDonald, L.

Nature 390, 364-370, 1997

A:Authors: Uterback, T.; Cotton, M.D.; Spriggs, T.; Artach, P.; Raine, B.P.; Sykes,

Smith, H.O.; Moese, C.R.; Venter, J.C.

A>Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing arch

A:Reference number: A69250; MUID:98049343; PMID:9389475

A:Accession: B69433

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-222 <KLE>

A:Cross-references: GB:AE001001; GB:AE000782; NID:g2689324; PIDN:AA89779.1; PID:g264

Query Match	Score	DB	Length
Best Local Similarity	43.18	2	222
Matches	6	Conservative	4; Mismatches
		Indels	0; Gaps
			0;

OY 3 SZPCGAVMILYF 14

DB 204 NEPCGAVFMEF 215

RESULT 2

A47439 gamma-glutamyl carboxylase (EC 4.1.1.-) - bovine

C:Species: Bos primigenius taurus (cattle)

C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999

C/Accession: A47439; A38939; B39283; C39283

R:Rehntulla, A.; Roth, D.A.; Wasley, L.C.; Kuliopulos, A.; Walsh, C.T.; Furie, B.; F

Proc. Natl. Acad. Sci. U.S.A. 90, 4611-4615, 1993

A>Title: In vitro and in vivo functional characterization of bovine vitamin K-depende

A:Reference number: A47439; MUID:93281629; PMID:8506307

A:Accession: A47439

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-758 <REH>

A:Cross-references: GB:U09726; NID:g289398; PIDN:AAA30425.1; PID:g289399

R:Wu, S.M.; Cheung, W.F.; Frazier, D.; Stafford, D.W.

Submitted to GenBank, January 1992

A:Reference number: A38939

A:Accession: A38939

A:Molecule type: mRNA

A:Residues: 96-758 <WUA>

A:Cross-references: GB:M81993; NID:g162744; PIDN:AAA30410.1; PID:g162745

R:Wu, S.M.; Cheung, W.F.; Frazier, D.; Stafford, D.W.

Science 254:1634-1636, 1991
 A:Title: Cloning and expression of the cDNA for human gamma-glutamyl carboxylase
 A:Reference number: A39283; MUID:92086658; PMID:1749535
 A:Accession: B39283
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 96-693, 695-758 <MU2>
 A:Cross-references: GB:M81593
 A:Accession: C39283
 A:Molecule type: protein
 A:Residues: 37-50 <MU3>
 C:Keywords: carbon-carbon lyase; carboxy-lyase

Query Match	43.1%	Score 44	DB 2	Length 758
Best Local Similarity	46.7%	Pred. NO. 22		
Matches 7	Conservative 2	Mismatches 6	Indels 0	Gaps 0
1	BTSZPCGAVMLTYH	15		
	: : : : : :			
Db	273 DASRPICGEVSYFH	287		

```

RESULT 3
AC2277
Hypothetical protein asr3770 [Imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp.
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
C:Accession: AC2277
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kurlitz, T.; Sasamoto, S.; Watanabe, A.; Iriuchihara, N.; Shimizu, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena PCC 7120
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AC2277
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-64 <KUR>
A:Cross-references: GB:BA000019; PIDN:BA875469.1; PID:g17132904; GSPDB:GN00179
A:Experimental source: strain PCC 7120
C:Genetics:
I:Gene: asr3770

```

```

Query Match      42.2% Score 43 DB 2 Length 64;
Best Local Similarity 58.3% Pred. No. 3.5;
Matches 7; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY      6 CGAAMLYFHKM 17
         |||  |||  |
Db       12 CGGVREKRYFW 23

RESULT 4
G71266
probable ATP-dependent nuclease, subunit A - syphilis spirochete
C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C:date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 05-Nov-1999
C:Accession: G71266

```

A:Title: Complete genome sequence of *Treponema pallidum*, the syphilis spirochete.
A:Reference number: A71250; MUID:98332770; PMID:9665876
A:Accession: G71266

A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-1239 <COL>
A:Cross-references: GB:AE001259; GB:AE000520; NID:33323209; PIDN:AMC65853.1; PID:g3332321
A:Experimental source: strain Nichols
A:Genetics:
A:Gene: TP0898

Query Match	42.28;	Score 43;	DB 2;	Length 1239;
Best Local Similarity	53.38;	Pred. No. 52;		
Matches	8;	Conservative	1;	Mismatches 6;
				Indels 0;
				Gaps 0;

```

OY      2 TSZPCGAVMILYFHK 16
          | ||| | : ||
Db      833 TDRACGAVQIMSVHK 847

```

RESULT 5
D86600
SET domain protein (Imported) - Chlamydomonas reinhardtii (strain J138)

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001
C:Accession: D86600
R:Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.
Nucleic Acids Res. 28, 2311-2314, 2000
A:Title: Completion of whole genome sequences of chlamydia pneumoniae J138.
A:Reference number: AB6491; MUID:2030349; PMID:10871362

A:Accession: D86b00
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-221 (5'>3')
A:Cross-references: GB:BA000008, NID:98979252, PID:BA99086.1, GSFDB:GN00142
A:Experimental source: strain J138
C:Genetics:
A:Gene: CPJ0878

Query Match	41.28;	Score 42;	DB 2;	Length 221;
Best Local Similarity	35.38;	Pred. No. 16;		
Matches	6;	Conservative	5;	Mismatches 6;
				Indels 0;
				Gaps 0;

```

OY      2 TS2PCGAVMILYFHKWR 18
         |::||::|::|
Db      5 TTEPCSSIHISLNDWR 21

```

RESULT 6
B01514

conserved hypothetical protein CP091 (imported) - Chlamydia pneumoniae (strain 1688) [Chlamydia pneumoniae] (strain 1688)
C:Species: Chlamydia pneumoniae, Chlamydia pneumoniae
C:Date: 31-Mar-2000 #sequence.revision 31-Mar-2000 #text.change 11-May-2000
C:Accession: B81514
R:Reed, T.D.; Brunning, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey
C:; Dodson, R.; Gwinn, M.; Nelson, W.; Deboy, R.; Kolonay, J.; McClarty, G.; Salzberg
Nucleic Acids Res. 28, 1397-1406, 2000
A:Title: Genome sequences of Chlamydia trachomatis Moyn and Chlamydia pneumoniae AR39
#:Reference number: A81500; MUID:20150253; PMID:10664935

A:Accession: BB1514
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-221 <REA>
A:Cross-references: GB:AE002257; GB:AE002161; MID:97189902; PIDN:AAF38770.1; PID:9718
A:Experimental source: strain AR39, HL cells
C:Genetics:
A:Gene: CP0991

Query Match	41.28;	Score 42;	DB 2;	Length 221;
Best Local Similarity	35.38;	Pred. NO. 16;		
Matches	6;	Conservative	5;	Mismatches 6;
				Indels 0;
				Gaps 0

```
QY      2 TS2PCGAVMILYFHWR 18
        |::|::|      :  ||
Db      5 TTEPCSSIHISLNDWR 21
```

RESULT 7

D72024

C:Accession: D72024
C:Domain: protein - Chlamydomonas reinhardtii (strain CWL029)
C:Species: Chlamydomonas reinhardtii, Chlamydomonas reinhardtii
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 05-May-2000
C:Author: Kallman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood,

Nature Genet. 21, 385-389, 1999
A:Title: Comparative genomes of *Campylobacter pneumoniae* and *C. trachomatis*.
A:Reference number: A72000; MUID:99206606; PMID:10192388
A:Accession: D72024
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-221 <ARN>
A:Cross-references: GB:AE001668; GB:AE001363; NID:94377192; PIDN:AAD19016.1; PID:9437719
A:Experimental source: strain CM1029
C:Genetics:
A:Gene: Cpn0878

Query Match 41.2%; Score 42; DB 2; Length 221;
Best Local Similarity 35.3%; Pred. No. 16;
Matches 6; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 2 TSZPCGAWMLYFHKMR 18
Db 5 TTEPCSSIHSLNMDMR 21

RESULT 8
AE0958
probable *lysR*-family transcriptional regulator STY3944 [imported] - *Salmonella enterica*
A:Title: *Salmonella enterica* subsp. *enterica* serovar typh
Note: This species has also been called *Salmonella typhi*
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
C:Accession: AE0958
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Garra, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skellon, J.; Stevens, K.; A:Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serovar
A:Reference number: AB0502; PMID:11677608
A:Accession: AE0958
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-302 <PAR>
A:Cross-references: GB:ALJ3382; PIDN:CAD03161.1; PID:916504796; GSPDB:GN00176
C:Genetics:
A:Gene: STY3944

Query Match 41.2%; Score 42; DB 2; Length 302;
Best Local Similarity 77.8%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 10 MLYFHKMR 18
Db 262 MLYFHKMR 270

ULT 9
589
conserved hypothetical protein PA0451 [imported] - *Pseudomonas aeruginosa* (strain PA01)
C:Species: *Pseudomonas aeruginosa*
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: H83589
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Braden, S.; Yun, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, N.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pathogen
A:Reference number: AB2950; MUID:2043737; PMID:10984043
A:Accession: H83589
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-443 <STO>
A:Cross-references: GB:AE004482; GB:AE004091; NID:99946303; PIDN:AMC03940.1; GSPDB:GN001
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA0451
C:Superfamily: Ribzodium nodulation competitiveness protein nfeD

Query Match 41.2%; Score 42; DB 2; Length 443;
Best Local Similarity 27.8%; Pred. No. 30;
Matches 5; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 BTSPCGAWMLYFHKMR 18
Db 393 DSEPCGAWMLYFHKMR 410

RESULT 10
D84686
probable RAD51B-like DNA repair protein [imported] - *Arabidopsis thaliana*
C:Species: *Arabidopsis thaliana* (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C:Accession: D84686
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shee, T.P.; Beito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, E.; D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.
A:Reference number: AB4420; MUID:20083487; PMID:10617197
A:Accession: D84686
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-353 <STO>
A:Cross-references: GB:AE002093; NID:94510403; PIDN:AAD21490.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g28560
A:Map position: 2

Query Match 40.2%; Score 41; DB 2; Length 353;
Best Local Similarity 53.3%; Pred. No. 36;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 TSZPCGAWMLYFHKMR 16
Db 60 TSPCGAVSVSLFFK 74

RESULT 11
T09771
phosphatidate cytidyltransferase (EC 2.7.7.41) - *Mycoplasma genitalium*
N:Alternate names: CDP-diglyceride synthetase
C:Species: *Mycoplasma genitalium*
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 02-Jun-2000
C:Accession: T09771; C64248
R:Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.; M.; Fuhmann, J.L.; Nguyen, D.T.; Utterback, T.; Saudek, D.M.; Phillips, C.A.; Merrick, C.A.; Venter, J.C.
Science 270, 397-403, 1995
A:Title: The minimal gene complement of *Mycoplasma genitalium*.
A:Reference number: A64200; MUID:96026346; PMID:7569993
A:Accession: C64248
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 70-374 <TIGR>
A:Cross-references: GB:U39730; GB:U43967; NID:91046149; PIDN:AB01627.1; PID:91046154
A:Experimental source: strain G-37
C:Genetics:
A:Gene: MG437
A:Genetic code: SGC3

C:Keywords: nucleotidyltransferase

Query Match 40.2%; Score 41; DB 2; Length 374;
Best Local Similarity 45.5%; Pred. No. 38;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 7 GAVMILYFHKW 17
DB 103 GTEVVVYFKW 113

RESULT 12

T05952

Mlo-hl protein - barley

C:Species: Hordeum vulgare (barley)

C>Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 15-Jun-2001

Accession: T05952

,Pantluga, R.

submitted to the EMBL Data Library, May 1997

A:Reference number: Z15093

A:Accession: T05952

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-344 <PAN>

A:Cross-references: EMBL:Z95496; PIDN:CAB08860.1

A:Experimental source: cv. Igrl

C:Genetics:

A:Gene: Mlo-hl

A:Map position: 4H

A:Insertions: 41/3; 139/3; 178/3; 199/1; 282/2; 289/1; 312/3; 382/3

C:Superfamily: barley pathogen resistance protein Mlo

Query Match 40.2%; Score 41; DB 2; Length 544;
Best Local Similarity 40.0%; Pred. No. 53;
Matches 10; Conservative 1; Mismatches 0; Indels 14; Gaps 1;

OY 8 AVMIL-----YFHKW 18
DB 23 AVMILSVAMEHALKLGHEFHKW 47

RESULT 13

T30418

Chitinase (EC 3.2.1.14) - *Lymantria dispar* nuclear polyhedrosis virus

C:Species: *Lymantria dispar* nuclear polyhedrosis virus, LdMNPV

C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 21-Jul-2000

C:Accession: T30418

R;Kuzlo, J.; Pearson, M.N.; Harwood, S.H.; Funk, C.J.; Evans, J.T.; Slavicek, J.M.; Rohlf

Virology 253, 17-34, 1999

A>Title: Sequence and analysis of the genome of a baculovirus pathogenic for *Lymantria c*

A:Reference number: Z20836; MUID:99124785; PMID:9887315

A:Accession: T30418

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-558 <KU2>

A:Cross-references: EMBL:AF081810; NID:93822234; PIDN:AC70356.1; PID:93822305

C:Function:

A:Description: catalyzes the hydrolysis of chitin, a beta-1,4-linked homopolymer of N-ac

A:Pathway: chitin degradation

C:Superfamily: Serratia marcescens chitinase

C:Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 40.2%; Score 41; DB 2; Length 558;
Best Local Similarity 40.0%; Pred. No. 54;
Matches 6; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

OY 3 SZPGAVMILYFHKW 17
DB 145 AEPYGVVAAVFEVW 159

RESULT 14

AB1793

ABC transporter (ATP-binding protein) homolog lin2888 [Imported] - *Listeria innocua* (

C:Species: *Listeria innocua*

C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001

C:Accession: AB1793

R;Glaeser, P.; Frangoul, L.; Buchtleier, C.; Amend, A.; Baquero, F.; Berche, P.; Bloec

; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihl,

D.; Jones, L.M.; Karst, U.

Science 294, 849-852, 2001

A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkut, G.; Madueno, E.; Maltournam, A.;

Ok, C.; Schluteter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehla

A>Title: Comparative genomics of *Listeria* species

A:Reference number: AB1077; MUID:21537279; PMID:11679669

A:Accession: AB1793

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-575 <GLA>

A:Cross-references: GB:AL592022; PIDN:CAC98114.1; PID:g16415423; GSPDB:GN00178

A:Experimental source: strain C1P11262

C:Genetics:

A:Gene: lin2888

C:Superfamily: Escherichia coli ABC transporter mlaA; ATP-binding cassette homology

Query Match 40.2%; Score 41; DB 2; Length 575;
Best Local Similarity 50.0%; Pred. No. 56;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 7 GAVMILYFHKW 18
DB 150 GATILFFMDWK 161

RESULT 15

AH1417

ABC transporter (ATP-binding protein) homolog lmo2745 [Imported] - *Listeria monocytog*

C:Species: *Listeria monocytogenes*

C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001

C:Accession: AH1417

R;Glaeser, P.; Frangoul, L.; Buchtleier, C.; Amend, A.; Baquero, F.; Berche, P.; Bloec

; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihl,

D.; Jones, L.M.; Karst, U.

Science 294, 849-852, 2001

A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkut, G.; Madueno, E.; Maltournam, A.;

Ok, C.; Schluteter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehla

A>Title: Comparative genomics of *Listeria* species.

A:Reference number: AB1077; MUID:21537279; PMID:11679669

A:Accession: AH1417

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-575 <GLA>

A:Cross-references: GB:NC_003210; PIDN:CAD00958.1; PID:g16412245; GSPDB:GN00177

A:Experimental source: strain EGD-e

C:Genetics:

A:Gene: lmo2745

C:Superfamily: Escherichia coli ABC transporter mlaA; ATP-binding cassette homology

Query Match 40.2%; Score 41; DB 2; Length 575;
Best Local Similarity 50.0%; Pred. No. 56;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 7 GAVMILYFHKW 18
DB 150 GATILFFMDWK 161

Search completed: November 15, 2002, 11:44:35
Job time : 17 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 15, 2002, 11:43:09 ; Search time 11 Seconds

(Without alignments)
67.870 Million cell updates/sec

Title: US-09-881-569A-2

Perfect score: 102

Sequence: 1 BRSZPCGAVMLYFKMR 18

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

112892

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	ID	Description
1	45	44.1	758	1 VKGC_RAT	088496 ratius norv
2	44	43.1	758	1 VKGC_BOVIN	007175 bos taurus
3	41	40.2	305	1 CDSA_MYCGE	049433 m putative
4	41	40.2	544	1 MLH1_HORVU	049873 hordum vul
5	40	39.2	60	1 IBPS_BOVIN	P00975 bos taurus
6	40	39.2	100	1 YB02_YEAST	P28223 saccharomyc
7	40	39.2	272	1 Y415_MYCGE	P47655 mycoplasma
8	40	39.2	531	1 UD13_RAT	064637 rattus norv
9	40	39.2	830	1 PKN2_MYXXA	P54736 myxococcus
10	39.5	38.7	438	1 IRX6_MOUSE	Q5875 mus musculus
11	39	38.2	148	1 YN32_ARCFU	Q27952 archaeglob
12	39	38.2	284	1 UPK_LACIA	Q36047 lactococcus
13	39	38.2	388	1 YBL2_SEV3L	P27403 simian foam
14	39	38.2	422	1 YURO_BACSU	Q32156 bacillus su
15	39	38.2	1147	1 KIN2_YEAST	P13166 saccharomyc
16	38.5	37.7	75	1 IAA2_STROI	P20536 streptomyce
17	38.5	37.7	227	1 COX2_DAMUA	P28032 daubentonia
18	38.5	37.7	1724	1 PPOV_HUMAN	Q94833 homo sapien
19	38	37.3	100	1 BPT2_BOVIN	Q17025 anopheles g
20	38	37.3	258	1 CTR2_ANGOA	P50173 pseudomonas
21	38	37.3	365	1 GLDA_PSEPU	Q32972 chlamydia p
22	38	37.3	1043	1 SYL_CHELPN	P28890 felis silve
23	37.5	36.8	322	1 COX2_FELCA	Q29502 archaeglob
24	37.5	36.8	122	1 PPAC_ARCFU	Q29502 archaeglob
25	37	36.3	122	1 YB02_YEAST	Q66452 aquifex aeo
26	37	36.3	168	1 NADP_AOUAE	Q37568 streptococc
27	37	36.3	281	1 UPK_STRPN	P77183 escherichia
28	37	36.3	318	1 YAGQ_ECOLI	P97401 mus musculu
29	37	36.3	323	1 FRZB_MOUSE	Q95117 bos taurus
30	37	36.3	325	1 FRZB_BOVIN	Q92765 homo sapien
31	37	36.3	359	1 FRZB_HUMAN	Q69555 mycobacteri
32	37	36.3	359	1 MRAY_MYCLE	Q00633 homo sapien
33	37	36.3	403	1 PTEN_HUMAN	008586 mus musculu

34	37	36.3	403	1	PTEN_MOUSE	008586	mus musculu
35	37	36.3	429	1	YQ84_MYCTU	Q07186	mycobacteri
36	37	36.3	432	1	Y672_MERYU	Q58066	methanococc
37	37	36.3	461	1	ENGA_MYCLE	Q49884	mycobacteri
38	37	36.3	502	1	C72G_ARATH	Q91747	arabidopsis
39	37	36.3	536	1	ZPB_PIG	Q07287	sus scrofa
40	37	36.3	661	1	PDAT_YEAST	P40345	saccharomyc
41	37	36.3	831	1	VPPI_HUMAN	Q93050	homo sapien
42	37	36.3	838	1	VPPI_BOVIN	Q29466	bos taurus
43	37	36.3	838	1	VPPI_RAT	P25286	rattus norv
44	37	36.3	839	1	VPPI_MOUSE	Q92164	mus musculu
45	37	36.3	862	1	AXN1_HUMAN	Q15169	homo sapien

ALIGNMENTS

RESULT 1	QUERY	STANDARD	PRT	758 AA
1	VKGC_RAT			
AC	088496;			
DT	15-DEC-1998 (Rel. 37, Created)			
DT	15-DEC-1998 (Rel. 37, Last sequence update)			
DT	15-DEC-1998 (Rel. 37, Last annotation update)			
DE	Vitamin K-dependent gamma-carboxylase (EC 6.4.-.-) (gamma-glutamyl carboxylase).			
GN	GCX.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_TaxID=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Sprague-Dawley; Tissue=Liver;			
RX	MEDLINE=98369628; Pubmed=9704005;			
RA	Romero E.E., Deo R., Velazquez-Estades L.J., Roth D.A.;			
RT	*Cloning, structural organization, and transcriptional activity of the rat vitamin K-dependent gamma-glutamyl carboxylase gene.*;			
RL	Biochem. Biophys. Res. Commun. 248:783-788(1998).			
RM	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Sprague-Dawley; Tissue=Liver;			
RX	MEDLINE=98417574; Pubmed=9743593;			
RA	Romero E.E., Velazquez-Estades L.J., Deo R., Schapiro B., Roth D.A.;			
RT	*Cloning of rat vitamin K-dependent gamma-glutamyl carboxylase and developmentally regulated gene expression in post-implantation embryos.*;			
RL	Exp. Cell Res. 243:334-346(1998).			
CC	-1- PUNCTION: VITAMIN K-DEPENDENT CARBOXYLATION OF MULTIPLE AMINO-TERMINAL GLUTAMIC ACID RESIDUES IN VARIOUS PROTEINS, IT CONVERTS			
CC	GLUTAMATE RESIDUES TO GAMMA-CARBOXYGLUTAMATE.			
CC	-1- SUBUNIT: MAY FORM A HOMODIMER (PROBABLY).			
CC	-1- SIMILARITY: SOME, TO PLANT AND MAMMALIAN LIPPOXYGENASES.			
CC	-----			
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CC	or send an email to license@isb-sib.ch .			
DR	EMBL: AF065387; AAC82374.1; -			
DR	EMBL: AF065387; AAC82374.1; -			
DR	InterPro: IPR001870; Gamma_carboxylase.			
DR	Ligase.			
SO	SEQUENCE 758 AA; 87478 MW; 6CF2FC8DC96A71A1 CRC64;			
QY	Query Match	44.1%	Score 45;	DB 1; Length 758;
	Best Local Similarity	46.7%	Pred. No. 6.5;	
	Matches	7;	Conservative	2; Mismatches 6; Indels 0; Gaps 0;
	1 BRSZPCGAVMLYFKMR 15			

DB 273 DASRPIGLVFSYFH 287

RESULT 2

WKCC_BOVIN STANDARD: PRT: 758 AA.

AC 007175;

DT 01-OCT-1994 (Rel. 30, Created)

DT 01-OCT-1994 (Rel. 30, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)

DE Vitamin K-dependent gamma-carboxylase (EC 6.4.-.-) (Gamma-glutamyl carboxylase).

DE GGCX OR GC.

GN Bos taurus (Bovine).

OS Bos taurus; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.

NCBI_TaxID=9913;

NCBI_TaxID=9913;

RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RC TISSUE=Liver;

RX MEDLINE=93281629; PubMed=8506307;

RA Rehentulla A., Roch D.A., Masley L.C., Kulipulos A., Walsh C.T., Furlie B., Furlie B.C., Kaufman R.J.;

RT "In vitro and in vivo functional characterization of bovine vitamin K-dependent gamma-carboxylase expressed in Chinese hamster ovary cells."

RT Proc. Natl. Acad. Sci. U.S.A. 90:4611-4615(1993).

RL (12)

RP SEQUENCE OF 96-758 FROM N.A., AND PARTIAL SEQUENCE.

RC TISSUE=Liver;

RX MEDLINE=92086858; PubMed=1749935;

RA Wu S.-M., Cheung W.-F., Frazier D., Stafford D.W.;

RT "Cloning and expression of the cDNA for human gamma-glutamyl carboxylase."

RT Science 254:1634-1636(1991).

CC -1- FUNCTION: VITAMIN K-DEPENDENT CARBOXYLATION OF MULTIPLE AMINO-TERMINAL GLUTAMIC ACID RESIDUES IN VARIOUS PROTEINS, IT CONVERTS GLUTAMATE RESIDUES TO GAMMA-CARBOXYGLUTAMATE.

CC -1- SUBUNIT: MAY FORM A HOMODIMER (PROBABLE).

CC -1- PTM: THE N-TERMINUS IS BLOCKED.

CC -1- SIMILARITY: SOME, TO PLANT AND MAMMALIAN LITOXENASES.

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CC EMBL: L09726; AAA30425.1; -

DR EMBL: M81593; AAA30410.1; -

DR InterPro: IPR001870; Gamma_Carboxylase.

KW Ligase.

SQ SEQUENCE 758 AA; 87557 MW; 9B7F47B809D1A873 CRC64;

Query Match 43.1%; Score 44; DB 1; Length 758;

Best Local Similarity 46.7%; Pred. No. 9.6;

Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 1 B7S2PCGAVMILYFH 15

DB 273 DASRPIGLVFSYFH 287

RESULT 3

CDSA_MYCGE STANDARD: PRT: 305 AA.

AC 049433; 049309;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Putative phosphatidate cytidyltransferase (EC 2.7.7.41) (CDP-diglyceride synthetase) (CDP-diglyceride pyrophosphorylase) (CDP-diacylglycerol synthase) (CDS) (CTP:phosphatidate cytidyltransferase) (CDP-DAG synthase) (CDP-DG synthetase).

GN CDSA OR MG437.

OS Mycoplasma genitalium.

OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.

NCBI_TaxID=2097;

NCBI_TaxID=2097;

RP SEQUENCE FROM N.A.

RC STRAIN=ATCC 33530 / G-37;

RX MEDLINE=96026346; PubMed=7569993;

RA Fraser C.M., Cocayne J.D., White O., Adams M.D., Clayton R.A., Fleischmann R.D., Bull C.J., Kerlavage A.R., Sutton G., Kelley J.M., Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L., Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M., Tomb J.-F., Dougherty B.A., Bort K.F., Hu P.-C., Lueder T.S., Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;

RT "The minimal gene complement of Mycoplasma genitalium."

RT Science 270:397-403(1995).

RL (12)

RP SEQUENCE OF 127-226 FROM N.A.

RC STRAIN=ATCC 33530 / G-37;

RX MEDLINE=94075230; PubMed=8253680;

RA Peterson S.N., Hu P.-C., Bort K.F., Hutchison C.A. III;

RT "A survey of the Mycoplasma genitalium genome by using random RT sequencing."

RT J. Bacteriol. 175:7918-7930(1993).

CC -1- CATALYTIC ACTIVITY: CTP + phosphatidate = diphosphate + CDP-diacylglycerol.

CC -1- PATHWAY: Phospholipid biosynthesis.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).

CC -1- SIMILARITY: BELONGS TO THE CDS FAMILY.

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CC EMBL: U39725; AAC72458.1; ALT_INIT.

DR EMBL: U02189; AAD12473.1; -

DR TIGR: MG437; -

DR InterPro: IPR000374; Pcttransf.

DR Pfam: PF01148; Cytidylyltrans. 1.

DR PROSITE: PS01315; CDS.1.

KW Hypothetical protein; Transferase; Nucleotidyltransferase; Phospholipid biosynthesis; Transmembrane; Complete proteome.

KW TRANSMEM 22

FT TRANSMEM 51 71

FT TRANSMEM 84 104

FT TRANSMEM 107 127

FT TRANSMEM 152 172

FT TRANSMEM 212 232

FT TRANSMEM 264 284

FT TRANSMEM 305 319

SQ SEQUENCE 305 AA; 34195 MW; F149FACBD9DDC080 CRC64;

Query Match 40.2%; Score 41; DB 1; Length 305;

Best Local Similarity 45.5%; Pred. No. 13;

Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 7 GAVMILYFHKM 17

DB 34 GTFVVFYFKM 44

RESULT 4

MLH1_HORVU STANDARD: PRT: 544 AA.

AC 049873;

DT 15-JUL-1999 (Rel. 38, Created)

DT 15-JUL-1999 (Rel. 38, last sequence update)
 DE MLO protein homolog 1.
 GN MLO-HL.
 OS Hordeum vulgare (Barley).
 OC Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:
 OC Spermatophyta: Magnoliophyta: Liliopsida: Poales: Poaceae: Pooidae:
 OC Triticeae: Hordeum.
 NCBI_TaxID=4513;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Igrl.
 RA Panstruga R.
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -1- SIMILARITY: BELONGS TO THE MLO FAMILY.
 CC -----
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 EMBL: Z95496; CAB08860.1; -
 DR InterPro: IPR004326; MLO.
 DR Pfam: PF03094; MLO; 1.
 KW Transmembrane.
 FT TRANSMEM 16 36 POTENTIAL.
 FT TRANSMEM 285 305 POTENTIAL.
 FT TRANSMEM 403 423 POTENTIAL.
 SQ SEQUENCE 544 AA; 60875 MW; DAFBCDD2A2A67796 CRC64;
 Query Match 40.2%; Score 41; DB 1; Length 544;
 Best Local Similarity 40.0%; Pred. No. 22;
 Matches 10; Conservative 1; Mismatches 0; Indels 14; Gaps 1;
 QY 8 AVML-----YFKWR 18
 ID 23 AVMLVSVAMEHALKLGHPFKWR 47
 DB
 RESULT 5
 ID 1BPS_BOVIN STANDARD; PRT; 60 AA.
 AC P00975;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Serum basic protease inhibitor (Serum BPI).
 OS Bos taurus (Bovine).
 OC Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
 OC Mammalia: Eutheria: Cetartiodactyla: Ruminantia: Pecora: Bovidae:
 OC Bovidae: Bovinae: Bos.
 NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE.
 RA MEDLINE-81044408; PubMed-7428928;
 RX Wechter E., Deppner K., Hochstrasser K., Lempert K., Geiger R.
 RT "A new kunitz-type inhibitor from bovine serum amino acid sequence
 RT determination".
 RL FEBS Lett. 119:58-62(1980).
 CC -1- FUNCTION: THIS INHIBITOR HAS ACTIVITY VERY SIMILAR TO THAT OF THE
 CC BASIC PROTEASE INHIBITOR FROM BOVINE TISSUES.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
 CC PIR: A01206; TIBOR.
 DR HSSP: P00974; IBPI.
 DR InterPro: IPR002223; Kunitz_BPTI.
 DR Pfam: PF00014; Kunitz_BPTI; 1.
 DR PRINTS: PR00759; BASICPTASE.
 DR PRODOM: PD000222; Kunitz_BPTI; 1.

DR SMART: SM00131; KU; 1.
 DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE: PS50279; BPTI_KUNITZ_2; 1.
 KW Serine protease inhibitor.
 FT DISULFID 7 57 BY SIMILARITY.
 FT DISULFID 16 40 BY SIMILARITY.
 FT DISULFID 32 53 BY SIMILARITY.
 FT ACT_SITE 17 18 REACTIVE BOND.
 SQ SEQUENCE 60 AA; 6647 MW; B9953EBAACF1A4E6 CRC64;
 Query Match 39.2%; Score 40; DB 1; Length 60;
 Best Local Similarity 63.6%; Pred. No. 3.7;
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 5 PCGAVMLYFPH 15
 ID 15 PCGAVMLYFPH 25
 DB
 RESULT 6
 ID YB02_YEAST STANDARD; PRT; 100 AA.
 AC P38223;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Hypothetical 11.5 kDa protein in RPL4A-HMT1 intergenic region.
 GN YBR032W OR YBR0317.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota: Fungi: Ascomycota: Saccharomycotina: Saccharomycetes:
 OC Saccharomycetales: Saccharomycetaceae: Saccharomyces.
 NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-S288c;
 RX MEDLINE-94378725; PubMed-8091864;
 RA Smits P.H.M., de Haan M., Maat C., Grievell L.A.;
 RT "The complete sequence of a 33 kb fragment on the right arm of
 RT chromosome II from Saccharomyces cerevisiae reveals 16 open reading
 RT frames, including ten new open reading frames, five previously
 RT identified genes and a homologue of the SC01 gene.";
 RL Yeast 10:S75-S80(1994).
 CC -----
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 DR EMBL: Z35901; CAA84974.1; -
 DR PIR: S45888; S45888
 DR SCD: S0000236; YBR032W.
 KW Hypothetical protein.
 SQ SEQUENCE 100 AA; 11485 MW; 1F24DEAC6C2793 CRC64;
 Query Match 39.2%; Score 40; DB 1; Length 100;
 Best Local Similarity 40.0%; Pred. No. 6.2;
 Matches 6; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
 QY 1 BPS2PCGAVMLYFPH 15
 ID 33 BPS2PCGAVMLYFPH 47
 DB
 RESULT 7
 ID Y415_MYCGE STANDARD; PRT; 272 AA.
 AC P47655;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)

```

DE Hypothetical protein MG415.
GN MG415.
OS Mycoplasma genitalium.
OC Bacteria: Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2097;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33530 / G-37;
RX MEDLINE=96026346; PubMed=7569993;
RA Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
RA Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,
RA Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhmann J.L.,
RA Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M.,
RA Tomb J.F., Dougherty B.A., Bolt K.F., Hu P.-C., Lueder T.S.,
RA Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;
RT "The minimal gene complement of Mycoplasma genitalium.";
Science 270:397-403(1995).
CC -1- SIMILARITY: BELONGS TO THE MG414 / MG415 FAMILY.
CC -----
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CC -----
DR EMBL: U39723; AAC71642.1; -.
DR TIGR: MG415; -.
DR Hypothetical protein; Transmembrane; Complete proteome.
KM TRANSMEM 233 253 POTENTIAL.
SQ SEQUENCE 272 AA; 32504 MW; A221BA6185231A4 CRC64;

Query Match 39.2%; Score 40; DB 1; Length 272;
Best Local Similarity 62.5%; Pred. No. 17;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 10 MILEFHKM 17
: |||||
Db 250 VEYFHKM 257

RESULT 8
D UD13_RAT STANDARD; PRT; 531 AA.
ID UD13_RAT
P 064637;
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE UDP-glucuronosyltransferase 1-3 precursor, microsomal (EC 2.4.1.17)
DE (UDPGLT) (UGT1*3) (UGT1-03) (UGT1A3) (B3).
GN UGT1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE OF 1-286 FROM N.A.
RC STRAIN=Mistar;
RX MEDLINE=95332265; PubMed=7608130;
RA Eml Y., Ikushiro S.I., Iyanagi T.;
RT "Drug-responsive and tissue-specific alternative expression of
RT multiple first exons in rat UDP-glucuronosyltransferase family 1
RT (UGT1) gene complex.";
RL J. Biochem. 117:392-399(1995).
RN [2]
RP SEQUENCE OF 287-531 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=90274676; PubMed=2112380;
RA Sato H., Koike O., Tanabe K., Kasahama S.;
RT "Isolation and sequencing of rat liver bilirubin UDP-
RT glucuronosyltransferase cDNA: possible alternate splicing of a common
RT primary transcript.";
```

```

RL Biochem. Biophys. Res. Commun. 169:260-264(1990).
CC -1- FUNCTION: UDPGLT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND
CC SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND
CC ENDOGENOUS COMPOUNDS.
CC -1- CATALYTIC ACTIVITY: UDP-glucuronate + acceptor = UDP + acceptor
CC beta-D-glucuronoside.
CC -1- SUBCELLULAR LOCATION: Microsomal.
CC -1- ALTERNATIVE PRODUCTS: THE UGT1 GENE ENCODES FOR MANY DIFFERENT
CC UDPGLT ISOZYMES WHICH HAVE A DIFFERENT N-TERMINAL DOMAIN AND A
CC COMMON C-TERMINAL DOMAIN OF 245 RESIDUES.
CC -1- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.
CC -----
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CC -----
DR EMBL: D38067; BAA07262.1; -.
DR EMBL: M34007; AAA2312.1; ALT-TERM.
DR InterPro: IPR002213; UDPGLT.
DR Pfam: PF00201; UDPGLT; 1.
DR PROSITE: PS00375; UDPGLT; 1.
KM Transferase; Glycosyltransferase; Glycoprotein; Transmembrane; signal;
KM Multigene family; Microsome; Alternative splicing.
FT SIGNAL 1 25 POTENTIAL.
FT CHAIN 26 531 UDP-GLUCURONOSYLTRANSFERASE 1-3.
FT TRANSMEM 489 505 POTENTIAL.
FT CARBOHYD 116 116 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 139 139 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 431 431 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 531 AA; 60140 MW; ECB0994C6AC7CEP CRC64;

Query Match 39.2%; Score 40; DB 1; Length 531;
Best Local Similarity 66.7%; Pred. No. 32;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 PCGAVMILY 13
|||||:|
Db 153 PCGAVLMY 161

RESULT 9
D PKN2_MYXXA STANDARD; PRT; 830 AA.
ID PKN2_MYXXA
P 954736;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Serine/threonine-protein kinase pkn2 (EC 2.7.1.1.-).
GN PKN2.
OS Myxococcus xanthus.
OC Bacteria; Proteobacteria; delta subdivision; Myxobacteria;
OC Myxococcales; Cytiobacterineae; Myxococcaceae; Myxococcus.
OX NCBI_TaxID=34;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DEF1;
RX MEDLINE=95293229; PubMed=7774814;
RA Udo H., Munoz-Dorado J., Inouye M., Inouye S.;
RT "Myxococcus xanthus, a Gram-negative bacterium, contains a
RT transmembrane protein serine/threonine kinase that blocks the
RT secretion of beta-lactamase by phosphorylation.";
RL Genes Dev. 9:972-983(1995).
CC -1- FUNCTION: REGULATES THE ACTIVITY OF ENDOGENOUS BETA-LACTAMASE OR
CC RELATED ENZYMES, BY BLOCKING THEIR SECRETION BY PHOSPHORYLATION,
CC IN RESPONSE TO AN EXTERNAL SIGNAL YET TO BE IDENTIFIED.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC -----
CC -1- SIMILARITY: CONTAINS 1 GUANYLATE CYCLASE DOMAIN.
```


Query Match 38.2%; Score 39; DB 1; Length 148;
 Best Local Similarity 41.2%; Pred. No. 13;
 Matches 7; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Qy 1 BRSZPCGAVMLYFHKW 17
 Db 54 DVQPTGKEIILCFPKW 70

RESULT 12

UPK_LACLA STANDARD: PRT: 284 AA.

AC 09CDM7;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Putative undecaprenol kinase (EC 2.7.1.66) (Bactitracin resistance protein).
 GN UPK OR BACA OR IL2192.
 OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
 OC Bacteria: Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
 OX NCBI_TaxID=1360;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=IL1403;
 RX MEDLINE=2135186; PubMed=11337471;
 RA Bolotin A., Munkner P., Manger S., Jallion O., Malarme K.,
 RA Weissbach J., Ehrlich S.D., Sorokin A.,
 RA "The complete genome sequence of the lactic acid bacterium Lactococcus
 RT lactis ssp. lactis IL1403.";
 RL Genome Res. 11:731-753(2001).
 CC -1- FUNCTION: Probably phosphorylates undecaprenol to undecaprenyl
 CC phosphate. Confers resistance to bactitracin (By similarity).
 CC -1- CATALYTIC ACTIVITY: ATP + undecaprenol -> ADP + undecaprenyl
 CC phosphate.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
 CC -1- MISCELLANEOUS: Bactitracin is thought to be involved in inhibition
 CC of peptidoglycan synthesis by sequestering undecaprenyl
 CC diphosphate reducing the pool of lipid carrier available.
 CC -1- SIMILARITY: BELONGS TO THE UPK FAMILY.

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 CC -----
 CC EMBL: AE006448; AAK06290.1; -;
 CC DR InterPro: IPR003824; BACA.2.
 CC DR pfam: PF02673; BACA.2.
 CC KW Transferrase; Kinase; Antibiotic resistance; Transmembrane;
 CC Complete proteome.
 CC FT TRANSMEM 7 29 POTENTIAL.
 CC FT TRANSMEM 44 66 POTENTIAL.
 CC FT TRANSMEM 86 108 POTENTIAL.
 CC FT TRANSMEM 118 137 POTENTIAL.
 CC FT TRANSMEM 158 180 POTENTIAL.
 CC FT TRANSMEM 195 217 POTENTIAL.
 CC FT TRANSMEM 229 251 POTENTIAL.
 CC FT TRANSMEM 266 283 POTENTIAL.
 CC SO SEQUENCE 284 AA; 32079 MW; 83ABD014DD0B14E CRC64;

Query Match 38.2%; Score 39; DB 1; Length 284;
 Best Local Similarity 66.7%; Pred. No. 26;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 8 AVMLYFHKW 16
 Db 57 SVVVLVYFHKW 65

Query Match 38.2%; Score 39; DB 1; Length 388;
 Best Local Similarity 60.0%; Pred. No. 35;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 8 AVMLYFHKW 17
 Db 243 AVKALHFHKW 252

RESULT 13

YBL2_SFV3L STANDARD: PRT: 388 AA.

AC P27403; Q88191;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE BEL-2 protein.
 GN BEL-2.
 OS Simian foamy virus (type 3 / strain UK3) (SFV-3).
 OC Viruses: Retroviridae; Retroviridae; Spumaviruses.
 OC NCBI_TaxID=11644;
 OX (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92124734; PubMed=1310187;
 RA Renne R., Friedl E., Schweizer M., Fleps U., Turek R.,
 RA Neumann-Haefelin D.,
 RA "Genomic organization and expression of simian foamy virus type 3
 RT (SFV-3)."
 RL Virology 186:597-608(1992).
 CC -1- FUNCTION: MIGHT BE IMPORTANT IN VIRAL LIFE CYCLE.

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 CC -----
 CC EMBL: M74895; AAA47800.1; -;
 CC DR EMBL: M74895; AAA47797.1; ALT_INIT.
 CC DR PIR: E40820; WMLJBT.
 CC DR InterPro: IPR004956; Foamy_BEL.
 CC DR pfam: PF03274; Foamy_BEL.1.
 CC KW Hypothetical protein.
 CC SO SEQUENCE 388 AA; 44527 MW; 45D6F74F3ED53966 CRC64;

Query Match 38.2%; Score 39; DB 1; Length 388;
 Best Local Similarity 60.0%; Pred. No. 35;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 8 AVMLYFHKW 17
 Db 243 AVKALHFHKW 252

YURO_BACSU STANDARD: PRT: 422 AA.

AC 032156;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Hypothetical ABC transporter extracellular binding protein yuro
 DE precursor.
 GN YURO.
 OS Bacillus subtilis.
 OC Bacteria: Firmicutes; Bacilliales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1423;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=98044033; PubMed=9384377;
 RA Kunz F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
 RA Azevedo V., Berteiro M.G., Bessieres P., Bolotin A., Borchert S.,
 RA Borris R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
 RA Brouillet S., Brusch C.V., Caldwell B., Capiano N.J., Carter N.M.,
 RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
 RA Denicot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
 RA Entian K.D., Errington J., Fabret C., Ferrari E., Fougere D.,
 RA Fritz C., Fujita M., Fujita Y., Fuma S., Gallizzi A., Gallier N.,

RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
 RA Giuseppe G., Guy B.J., Haga K., Hachez J., Harwood C.R., Henaut A.,
 RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
 RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
 RA Kobayashi Y., Koetter P., Koningsstein G., Kroch S., Kumano M.,
 RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
 RA Lee S.M., Levine A., Liu H., Masuda S., Malet C., Medigue C.,
 RA Medina N., Mellado R.P., Mizuno M., Moesti D., Nakai S., Noback M.,
 RA Noone D., O'Reilly M., Ogawa K., Ogihara A., Oudega B., Park S.H.,
 RA Paro V., Pohl T.M., Portetelle D., Porcullik S., Prescott A.M.,
 RA Plescan E., Puig C., Purnelle B., Rapoport G., Rey M., Reynolds S.,
 RA Rieger M., Rivoita C., Roche E., Roche B., Rose M., Sadate Y.,
 RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
 RA Sekiguchi J., Sekowska A., Seror S.J., Serro P., Shin B.S., Soldo B.,
 RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
 RA Takeuchi M., Tanakoshi A., Tanaka T., Terpsira P., Tognoni A.,
 RA Tsoato V., Uchiyama S., Vandenbol M., Vannier F., Vassart A.,
 RA Viari A., Wambutt R., Wedler E., Wedler K., Weitenegger T.,
 RA Winters P., Wiput A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
 RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.,
 RT "The complete genome sequence of the gram-positive bacterium *Bacillus*
 RL subtilis."

-1- FUNCTION: PROBABLY PART OF A BINDING-PROTEIN-DEPENDENT TRANSPORT
 SYSTEM YURMO.
 -1- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
 (potential).
 CC -1- SIMILARITY: BELONGS TO THE BACTERIAL EXTRACELLULAR SOLUTE-BINDING
 CC PROTEIN FAMILY 1.
 CC -----
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 CC -----
 DR EMBL: Z99120; CAB1250.1; -.
 DR Subtilist; BG14001; YURO.
 DR InterPro: IPR000567; SBP_pac_1.
 DR Pfam: PF01547; SBP_bacterial.1; 1.
 DR PROSITE: PS00013; PROKAR_LIPOPROTEIN_1.
 DR PROSITE: PS01037; SBP_BACTERIAL_1; FALSE_NEG.
 KW Hypothetical protein; Transport; Membrane; Lipoprotein; Signal;
 KW Complete proteome.
 FT SIGNAL 1 20
 FT CHAIN 1 422
 FT LIPID 21 21
 FT SEQUENCE 422 AA; 48026 MW; 49D67BDC787CF42E CRC64;
 SO

very March 38.2%; Score 39; DB 1; Length 422;
 est Local Similarity 37.5%; Pred. NO. 38;
 Matches 6; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

OY 2 TSZPCGAVMILYFKW 17
 Db 25 SSSADGKVTLEFFHRM 40

RESULT 15
 KIN2_YEAST STANDARD: PRT: 1147 AA.
 AC KIN2_YEAST Q12384;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE protein kinase KIN2 (EC 2.7.1.-).
 GN KIN2 OR YLR096W OR L8004.3.
 OS *Saccharomyces cerevisiae* (Baker's yeast).
 CC Eukaryota; Fungi; Ascomycota; *Saccharomycotina*; *Saccharomycetes*;
 CC *Saccharomycetales*; *Saccharomycetaceae*; *Saccharomyces*.

OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87317589; PubMed=2957690;
 RA Levin D.E., Hammond C.I., Ralston R.O., Bishop J.M.;
 RT "Two yeast genes that encode unusual protein kinases."
 RL Proc. Natl. Acad. Sci. U.S.A. 84:6035-6039(1987).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Benes V., Rehmman S., Nentwich U., Schwager C., Ansoerge W., Voss H.;
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=5288c / AB972;
 RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du Z.,
 RA Favelli A., Fulton L., Gattung S., Greco T., Kirsten J., Kucaba T.,
 RA Hallsworth K., Hawkins J., Hillier L., Jier M., Johnson D.,
 RA Johnston L., Langston Y., Latreille P., Le T., Madis E., Meneses S.,
 RA Miller N., Nnan M., Pauley A., Peluso D., Rifken L., Riles L.,
 RA Tatch A., Trevasakis E., Vignati D., Wilcox L., Wohlman P., Vaudin M.,
 RA Wilson R., Waterston R.;
 RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: THIS PROTEIN IS PROBABLY A SERINE/THREONINE PROTEIN
 CC KINASE.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC NIM1 SUBFAMILY.
 CC -----
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 CC -----
 DR EMBL: M69018; AAA34723.1; -.
 DR EMBL: Z73368; CAA97659.1; -.
 DR EMBL: Z73269; CAA97661.1; -.
 DR EMBL: U53876; AAB67540.1; -.
 DR PIR: S42439; S42439.
 DR HSSP: Q63450; 1A06.
 DR SGD: S0004086; KIN2.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR001772; Kinase_Cterm.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR Pfam: PF00069; pkinase_1.
 DR Pfam: PF02149; KAI; 1.
 DR ProDom: PD000001; Euk_pkinase; 1.
 DR SMART: SM00220; S_TKC_1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 KW Transferrase; Serine/threonine-protein kinase; ATP-binding.
 FT DOMAIN 99 377
 FT NP_BIND 105 113
 FT BINDING 128 128
 FT ACT_SITE 248 248
 FT DOMAIN 527 536
 FT CONFLICT 216 217
 FT CONFLICT 675 707
 FT

Query Match 38.2%; Score 39; DB 1; Length 1147;
 Best Local Similarity 43.8%; Pred. NO. 1e+02;
 Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

OY 1 BNSZPCGAVMILYFK 16

FT CONFLICT 756 758
 FT CONFLICT 805 805
 FT CONFLICT 1034 1037
 FT CONFLICT 1041 1042
 FT SEQUENCE 1147 AA; 128338 MW; AC2660BF3CA69600 CRC64;
 SO

REF. 1).
 NAE -> KRO (IN REF. 1).
 P -> PL5VP (IN REF. 1).
 ATNT -> TTNSI (IN REF. 1).
 NS -> KT (IN REF. 1).
 OH -> HD (IN REF. 1).
 OEPLREPTPTMSKNEISIKVPSKSRSTSD ->
 SGTYSKKNLCHICQNMKPFPSKYKAIVLVKOT (IN
 REF. 1).

Db 78 DASHKNGAVELEQFHR 93

Search completed: November 15, 2002, 11:43:30
Job time : 12 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 15, 2002, 11:43:14 ; Search time 29 Seconds
(without alignments)
127.891 Million cell updates/sec

Title: US-09-881-569A-2

Perfect score: 102

Sequence: 1 B7S2PCGAVMILYFKMR 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SPREMBL_21:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mammal:*
8: sp_mmc:*
9: sp_organelle:*
10: sp_phase:*
11: sp_plant:*
12: sp_rodent:*
13: sp_virus:*
14: sp_vertebrate:*
15: sp_unclassified:*
16: sp_virus:*
17: sp_bacteriophage:*
17: sp_archaeop:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	47.1	155	3	096033
2	46	45.1	326	5	095XA9
3	45	44.1	400	17	08TXF2
4	44	43.1	207	1	09V229
5	44	43.1	222	17	028805
6	44	43.1	333	16	08RG17
7	44	43.1	720	3	08X231
8	44	43.1	758	6	09GL59
9	44	43.1	894	10	08S4P5
10	43	42.2	64	16	08Y0Q0
11	43	42.2	992	2	08RTY6
12	43	42.2	992	2	08RTY5
13	43	42.2	1239	16	083868
14	42	41.2	79	2	09F569
15	42	41.2	221	16	09J529
16	42	41.2	221	16	09Z728

17	42	41.2	298	16	08ZRY5	08ZRY5 salmonella
18	42	41.2	302	16	08Z2N3	08Z2N3 salmonella
19	42	41.2	443	16	091667	091667 pseudomonas
20	42	41.2	602	3	08TFD3	08TFD3 mycoplasma
21	41.5	40.7	227	2	053090	053090 rhodospirillum rubrum
22	41.5	40.7	229	8	063548	063548 rhodospirillum rubrum
23	41	40.2	259	5	045048	045048 anopheles gambiae
24	41	40.2	317	17	097CM0	097CM0 thermoplasma
25	41	40.2	320	10	0945T6	0945T6 actinobaculum
26	41	40.2	353	10	09SK02	09SK02 arbidopsis
27	41	40.2	505	2	09R9S3	09R9S3 aeromonas
28	41	40.2	558	12	09YMQ7	09YMQ7 lymphocystis
29	41	40.2	575	16	09Z7A1	09Z7A1 listeria
30	41	40.2	575	16	08Y3T6	08Y3T6 listeria
31	41	40.2	612	16	09HU20	09HU20 pseudomonas
32	41	40.2	616	5	09N977	09N977 leishmania
33	41	40.2	746	5	016992	016992 ceanorhabditis
34	40.5	39.7	497	16	08XRY6	08XRY6 ralsomina
35	40.5	39.7	681	16	08XRY7	08XRY7 ralsomina
36	40.5	39.7	868	10	09SH67	09SH67 arabidopsis
37	40.5	39.7	954	5	095Y23	095Y23 leishmania
38	40.5	39.7	2133	12	098203	098203 molluscum
39	40	39.2	74	2	050168	050168 mycobacterium
40	40	39.2	156	5	08S0W8	08S0W8 encephalito
41	40	39.2	199	16	08U082	08U082 agrobacterium
42	40	39.2	257	10	09XFD1	09XFD1 thlocapsa
43	40	39.2	335	2	09L610	09L610 thlocapsa
44	40	39.2	450	2	046730	046730 escherichia
45	40	39.2	476	2	046731	046731 escherichia

ALIGNMENTS

RESULT 1

ID	096033	PRELIMINARY;	PRT;	155 AA.
AC	096033;			
DT	01-DEC-2001 (TREMBLrel. 19, Created)			
DR	01-DEC-2001 (TREMBLrel. 19, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	Hypothetical 17.5 kDa protein.			
OS	B208.030.			
GN	Neurospora crassa.			
OC	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;			
CC	Sordariaceae; Sordariaceae; Neurospora.			
OX	NCBI_TaxID=5141;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Schulte U., Algn V., Hohlseil J., Brandt P., Fartmann B., Holland R.,			
RA	Nyakatura G., Mewes H.W., Manhaupt G.;			
RL	Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	German Neurospora genome project;			
RA	Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.			
DR	EMBL: AL355930; CAP01121.1; -			
KW	Hypothetical protein.			
SO	SEQUENCE 155 AA; 17483 MW; 80E455D3BF0EC6AD CRC64;			
Query Match	47.1%; Score 48; DB 3; Length 155;			
Best Local Similarity	40.0%; Pred. No. 1.8;			
Matches	6; Conservative 4; Mismatches 5; Indels 0; Gaps 0;			
OY	4 B7S2PCGAVMILYFKMR 18			
DB	50 B7S2PCGAVMILYFKMR 64			
RESULT 2				
ID	095XA9	PRELIMINARY;	PRT;	326 AA.
AC	095XA9;			

DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Hypothetical 37.6 kDa protein.
 GN y20F4.3.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Pelodierinae; Caenorhabditis.
 OX NCBI_Taxid=6239;
 RN 11
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RA None;
 RT "Genome sequence of the nematode C. elegans: a platform for
 investigating biology. The C. elegans Sequencing Consortium.";
 RT Science 282:2012-2018(1998).
 LN 121
 NC SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Waterston R.;
 RT "Direct Submission."
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC093703; AL00863.1;
 DR InterPro: IPR000980; SH2.
 DR InterPro: IPR001452; SH3.
 DR Pfam: PF00017; SH2; 1.
 DR Pfam: PF00018; SH3; 1.
 DR PROSITE: PS50001; SH2; 1.
 DR PROSITE: PS50002; SH3; 1.
 DR Hypothetical protein.
 KW SEQUENCE 326 AA; 37576 MW; 5885F810848586CE CRC64;
 SQ
 Query Match 45.1%; Score 46; DB 5; Length 326;
 Best Local Similarity 53.8%; Pred. No. 7.8;
 Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
 OY 5 PCGAVMLTFHKW 17
 Db 61 PCSFSSISHFKW 73
 RESULT 3
 O8TXF2 PRELIMINARY; PRT: 400 AA.
 DT 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE CO dehydrogenase/acetyl-CoA synthase delta subunit (corrinoid Fe-S
 protein).
 GN CdhD OR MK0722.
 OS Methanopyrus kandleri.
 OC Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
 OC Methanopyrus.
 OX NCBI_Taxid=2320;
 RN 11
 RP SEQUENCE FROM N.A.
 RC STRAIN-AV19 / DSM 6324 / JCM 9639;
 RX MEDLINE=21927647; PubMed=11930014;
 RA Slesarev A.I., Mezheva K.V., Makova K.S., Polushin N.N.,
 RA Shchedrina O.V., Shakhova V.V., Belova G.I., Aravind L.,
 RA Natarle D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O.,
 RA Malykh A.G., Koonin E.V., Kozaykin S.A.;
 RT "The complete genome of hyperthermophile Methanopyrus kandleri AV19
 RT and monophyly of archaeal methanogens.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649(2002).
 RL EMBL: AB010365; AM01936.1;
 DR EMBL: AB010365; AM01936.1;
 KW Complete proteome.
 SQ SEQUENCE 400 AA; 44542 MW; 83ADA136E30C07CB CRC64;
 Query Match 44.1%; Score 45; DB 17; Length 400;
 Best Local Similarity 50.0%; Pred. No. 14;

Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 OY 6 CGAVMLTFHKW 17
 Db 361 CGADLMMFHKW 372
 RESULT 4
 O9V229 PRELIMINARY; PRT: 207 AA.
 AC O9V229;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-OCT-2001 (TREMBlrel. 18, Last annotation update)
 DE MCR4 (Fragment).
 GN MCR4.
 OS uncultured methanogen ODP8-ME2.
 OC Archaea; Euryarchaeota; Methanococci; Methanosarcinales;
 OC environmental samples.
 OX NCBI_Taxid=95922;
 RN 11
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99365980; PubMed=10436927;
 RA Bläse K.A., Kaster M., Bartlett D.H.;
 RT "A phylogenetic analysis of microbial communities associated with
 RT methane hydrate containing marine fluids and sediments in the Cascadia
 margin (ODP site 892B)."
 RL FEMS Microbiol. Lett. 177:101-108(1999).
 DR EMBL: AF121100; AF045632.1;
 DR HSP, P11558; IMRO.
 DR InterPro: IPR003183; MCR_alpha.
 DR Pfam: PF02249; MCR_alpha.
 DR Pfam: PF02745; MCR_alpha_N; 1.
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 207 AA; 22546 MW; 4A507ECA265D8621 CRC64;
 Query Match 43.1%; Score 44; DB 1; Length 207;
 Best Local Similarity 50.0%; Pred. No. 11;
 Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
 OY 4 ZPCGAVMLTFHKW 17
 Db 54 ETGCAAMLYDQIW 67
 RESULT 5
 O28805 PRELIMINARY; PRT: 222 AA.
 AC O28805;
 DT 01-JAN-1998 (TREMBlrel. 05, Created)
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Signal-transducing histidine kinase.
 GN Afi467.
 OS Archaeoglobus fulgidus.
 OC Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
 OC Archaeoglobaceae; Archaeoglobus.
 OX NCBI_Taxid=2234;
 RN 11
 RP SEQUENCE FROM N.A.
 RC STRAIN-VC-16 / DSM 4304 / ATCC 49558;
 RX MEDLINE=98049343; PubMed=9389475;
 RA Kleink H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
 RA Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
 RA Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
 RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
 RA Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
 RA Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,
 RA Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
 RA Cotton M.D., Spriggs T., Artach P., Kaine B.P., Sykes S.M.,
 RA Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
 RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,

RL Plant Physiol. 128:1332-1345(2002).
 DR EMBL: AF443597; AM13421.1; -
 SQ SEQUENCE 894 AA; 99979 MW; 9C2B04E6F80BA113 CRC64;

Query Match 43.1%; Score 44; DB 10; Length 894;
 Best Local Similarity 38.9%; Pred. No. 43;
 Matches 7; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 BTSPCGAVMLIFYHKWR 18
 : ||| : ||| :
 Db 317 ENKPCGCHLCYLRPPQWR 334

RESULT 10

ID 08Y000 PRELIMINARY; PRT; 64 AA.

DT 01-MAR-2002 (TREMBlrel. 20, Created)

DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)

DE Sphingolipid ceramide N-deacylase

OS Shewanella algae.

OC Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;

OC Anabaena sp. (strain PCC 7120).

OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.

OX NCBI_TaxID=103690;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=21595285; PubMed=11759840;

RA Kaneo T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,

RA Watanabe A., Iritaguchi M., Ishikawa A., Kawashima K., Kimura T.,

RA Kishida Y., Kohara M., Matsumoto K., Matsuno A., Muraki A.,

RA Nakazaki N., Shimpō S., Sugimoto M., Takazawa M., Yamada M.,

RA Yasuda M., Tabata S.;

RT "Complete genomic sequence of the filamentous nitrogen-fixing

RT cyanobacterium Anabaena sp. strain PCC 7120.";

RL DNA Res. 8:205-213(2001).

DR EMBL: AP003594; BAB75469.1; -

SW Hypothetical protein; Complete proteome.

QY SEQUENCE 64 AA; 7403 MW; 92AADC7A9C0F8E8 CRC64;

Query Match 42.2%; Score 43; DB 16; Length 64;
 Best Local Similarity 58.3%; Pred. No. 5.7;
 Matches 7; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

RESULT 11

ID 08RTY6 PRELIMINARY; PRT; 992 AA.

AC 08RTY6;

DT 01-JUN-2002 (TREMBlrel. 21, Created)

DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)

DE Sphingolipid ceramide N-deacylase.

OS Shewanella algae.

OC Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;

OC Shewanella.

OX NCBI_TaxID=38313;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=8;

RA Furusato M., Sueyoshi N., Mitsuake S., Sakaguchi K., Kita K.,

RA Okino N., Ichinose S., Omori A., Ito M.;

RT "Molecular Cloning and Characterization of Sphingolipid Ceramide N-

RT deacylase from a Marine Bacterium, Shewanella alga G8.";

RL J. Biol. Chem. 0:0-0(2002).

DR EMBL: AB079849; BAB85110.1; -

SO SEQUENCE 992 AA; 109848 MW; CECBCC6C7A2C6953 CRC64;

Query Match 42.2%; Score 43; DB 2; Length 992;

Best Local Similarity 34.8%; Pred. No. 70;
 Matches 8; Conservative 4; Mismatches 5; Indels 6; Gaps 1;

QY 2 TSPZPCGAVMLIFYH-----KWR 18
 : ||| : ||| :
 Db 967 SGE0AGALILYHHGDSNOKWK 989

RESULT 12

ID 08RTY5 PRELIMINARY; PRT; 992 AA.

DT 01-JUN-2002 (TREMBlrel. 21, Created)

DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)

DE Sphingolipid ceramide N-deacylase.

OS Shewanella algae.

OC Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;

OC Shewanella.

OX NCBI_TaxID=38313;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=NS589;

RA Sueyoshi N., Furusato M., Okino N., Mitsuake S., Ito M.;

RT "Molecular cloning and characterization of sphingolipid ceramide N-

RT deacylase from a marine bacterium, Shewanella alga NS589.";

RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL: AB079850; BAB85111.1; -

SO SEQUENCE 992 AA; 109862 MW; B7611F6B5DAE8BA CRC64;

Query Match 42.2%; Score 43; DB 2; Length 992;
 Best Local Similarity 34.8%; Pred. No. 70;
 Matches 8; Conservative 4; Mismatches 5; Indels 6; Gaps 1;

RESULT 13

ID 083868 PRELIMINARY; PRT; 1239 AA.

AC 083868;

DT 01-NOV-1998 (TREMBlrel. 08, Created)

DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)

DE ATP-dependent nuclelease, subunit A, putative.

OS Treponema pallidum.

OC Bacteria; Spirochaetales; Spirochaetaceae; Treponema.

OX NCBI_TaxID=160;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=NICHOLS;

RX MEDLINE=98332770; PubMed=9665876;

RA Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.C.,

RA Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A.,

RA Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,

RA Khalak H., Richardson D., Howell J.K., Chidambaram M., Uterback T.,

RA McDonald L., Artisch P., Bowman C., Cotton M.D., Fujii C., Garland S.,

RA Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,

RA Venter J.C.;

RT "Complete genome sequence of Treponema pallidum, the syphilis

RT spirochete.";

RL Science 281:375-388(1998).

DR EMBL: AE001259; AAC65853.1; -

DR HSSP: P09980; IUAA.

DR TIGR: TP0989; -

DR InterPro: IPR000212; UvrD-helicase.

DR Pfam: PF00580; UvrD-helicase; 1.

KW Complete proteome.

SO SEQUENCE 1239 AA; 137095 MW; DCCDA3B1F267597 CRC64;

Query Match 42.2%; Score 43; DB 16; Length 1239;
 Best Local Similarity 53.3%; Pred. No. 86;
 Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

OY 2 TSZPCGAVMIYFHKR 16
 DB 833 TDRACGAVOIMSVHK 847

RESULT 14

O9F569 PRELIMINARY: PRT: 79 AA.
 AC O9F569;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DE 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 GN YajB protein.
 OS Escherichia coli.
 OC Plasmid R721.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCB1_TaxID=562;
 [1]

SEQUENCE FROM N.A.
 STRAIN-K-12; TRANSPOSON-TN7;
 RA Stampel G., Motomura K., Masuda S., Yamaguchi T., Ando K., Oishi T.,
 RA Furuya N., Komano T., Mizobuchi K.;
 RT "Organization and diversification of plasmid genomes: complete
 RT nucleotide sequence of the R721 genome.";
 RL Submitted (JUN-2000) to the EMBL/Genbank/DBJ databases.
 RN [2]

RP SEQUENCE FROM N.A.
 RC STRAIN-K-12; TRANSPOSON-TN7;
 RX MEDLINE-93015772; PubMed-1400257;
 RA Kim S., Komano T.;
 RT "Nucleotide sequence of the R721 shuffle.";
 RL J. Bacteriol. 174:7053-7058(1992).
 DR EMBL; AP002527; BAB12599.1;
 KW Plasmid.
 SQ SEQUENCE 79 AA; 8923 MW; 091817FE76671D65 CRC64;

Query Match 41.2%; Score 42; DB 2; Length 79;
 Best Local Similarity 33.3%; Pred. No. 10;
 Matches 8; Conservative 4; Mismatches 4; Indels 8; Gaps 1;

OY 3 SZPCGA-----VMILYFHKR 18
 DB 47 SMPRALHECNCLYLMVFFEEWR 70

RESULT 15

O9J529 PRELIMINARY: PRT: 221 AA.
 AC O9J529;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DE 01-OCT-2001 (TREMBLrel. 18, Last annotation update)
 GN SET domain protein.
 GN CPJ0878 OR CP0991.
 OS Chlamydia pneumoniae (Chlamydia pneumoniae).
 OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
 OX NCB1_TaxID=83558;
 [1]

RP SEQUENCE FROM N.A.
 RC STRAIN-AR39;
 RX MEDLINE-20150255; PubMed-10684935;
 RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heideberg J.F.,
 RA White O., Hickey E.K., Peterson J., Ullback T., Berry K., Bass S.,
 RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
 RA Gwinn M., Nelson W., Deboy R., Kolonay J., McClarty G., Salzberg S.L.,
 RA Eisen J., Fraser C.M.;
 RT "Genome sequences of Chlamydia trachomatis Mopn and Chlamydia

RT pneumoniae AR39.";
 RL Nucleic Acids Res. 28:1397-1406(2000).
 RN [2]

RP SEQUENCE FROM N.A.
 RC STRAIN-J138;
 RX MEDLINE-20330349; PubMed-10871362;
 RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
 RA Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
 RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138
 RT from Japan and CWL029 from USA.";
 RL Nucleic Acids Res. 28:2311-2314(2000).
 DR EMBL; AE002257; AAF38770.1;
 DR EMBL; AP002548; BAA99086.1;
 DR TIGR; CP0991;
 DR InterPro: IPR001214; SET.
 DR Pfam: PF00856; SET; 1.
 DR SMART: SM00317; SET; 1.
 DR PROSITE: PS50280; SET; 1.
 SQ SEQUENCE 221 AA; 25889 MW; 4F6750E73FA08F6B CRC64;

Query Match 41.2%; Score 42; DB 16; Length 221;
 Best Local Similarity 35.3%; Pred. No. 26;
 Matches 6; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

OY 2 TSZPCGAVMIYFHKR 18
 DB 5 TTEPCSSIHISLNDWR 21

Search completed: November 15, 2002, 11:45:11
 Job time : 31 secs

